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Pred. No. is the number of results predicted by chance to have a

Result No.	Score	Query	Length	DB	ID	Description
1	1240.2	77.6	1626	12	AF401989	AR091989 Synthetic
2	1219.4	76.3	1623	6	AR091394	AR091394 Sequence
3	1219.4	76.3	6139	6	AR091393	AR091393 Sequence
4	1172.4	73.3	1560	6	AR091395	AR091395 Sequence
5	983.8	61.5	990	6	AR151071	AR151071 Sequence
6	983.8	61.5	990	6	E15017	E15017 Canine mRNA
7	977.4	61.1	1015	4	CFU49100	U49100 Canis fam11
8	969.4	60.6	990	6	AR151061	AR151061 Sequence
9	899.8	55.0	990	6	AX076200	AX076200 Sequence
10	879.8	55.0	1006	6	AX076482	AX076482 Sequence
11	879.8	55.0	1006	4	FC1112P40	Y07762 F. catus mRN
12	879.8	55.0	4522	6	AX076209	AX076209 Sequence
13	879.8	55.0	4522	6	AX076476	AX076476 Sequence
14	878.2	54.9	990	4	FCU83184	U83184 Felis catus
15	827	51.7	990	6	AX154603	AX154603 Sequence
16	811.2	50.7	1058	4	EC1112P40	Y11129 Equus caball
17	790.6	49.4	984	6	AX154600	AX154600 Sequence
18	785.8	49.1	984	6	AX154599	AX154599 Sequence
19	774.8	48.5	1669	12	AF411293	AF411293 Synthetic
20	773.6	48.4	1389	6	AX084106	AX084106 Sequence
21	772.6	48.3	987	6	AR008950	AR008950 Sequence
22	772.6	48.3	987	6	AX154633	AX154633 Sequence
23	772.6	48.3	987	6	BD007070	BD007070 IL-12 gen
24	772.6	48.3	987	6	BD007076	BD007076 Gene expr
25	772.6	48.3	987	6	I28591	I28591 Sequence 1
26	772.6	48.3	1007	9	AF180563	AF180563 Homo sapi
27	772.6	48.3	1018	6	AR052857	AR052857 Sequence
28	772.6	48.3	1399	6	AR091391	AR091391 Sequence
29	772.6	48.3	1399	9	HUMCMF40	M65272 Human cytlot
30	772.6	48.3	2362	6	AR082684	AR082684 Sequence
31	772.6	48.3	2362	6	AR122960	AR122960 Sequence
32	772.6	48.3	2362	6	I28325	I28325 Sequence 1
33	772.6	48.3	2362	6	I89770	I89770 Sequence 1
34	772	48.3	1080	9	MMU19841	U19841 Macaca mul
35	771	48.2	1870	6	A92079	A92079 Sequence 3
36	771	48.2	2318	9	HUMMSF40	M65290 Human natur
37	769.8	48.1	1012	4	AF007576	AF007576 Capra hir
38	766.6	47.9	984	4	AF209435	AF209435 Ovis arie
39	766.6	47.9	984	6	AX154598	AX154598 Sequence
40	763.4	47.7	984	4	AF004024	AF004024 Ovis arie
41	761.8	47.6	1012	4	BTU11815	U11815 Bos taurus
42	761.8	47.6	1012	4	E35794	E35794 Process for
43	760.2	47.5	993	4	CEU57752	U57752 Cervus elap
44	756.6	47.3	975	6	AX154597	AX154597 Sequence
45	756.6	47.3	1005	9	CTU19834	U19834 Cercopithec

Db	481	GGCTCTTCTGACCCCAAGGGGTGAGCTGGGGAGCTGCTACACTCTCTGCAAGAGAGTTC	540
QY	541	AGAGTGGGACACAGAGGATTTTAAAGAAAGTACACAGTGGAGTGTAGAGGGCGATGCTCGC	600
Db	541	AGAGGGGACACAGAGGATAT---GAGTACTCAGTGGAGTGCAGAGAGGACAGTCTCGC	597
QY	601	CCCTCTGCGGAGGAGAGCCATCCCATTCGAGGTCGTGGTGAATCTATTCCAAAGCTCAAG	660
Db	598	CCAGTCTGTGAGGAGAGTGTGCCCATTTGAGTGTGATGTGGTATGCCGTTCCAAAGCTCAAG	657
QY	661	TATGAAACCTACACCAGAGCTTCTTCATAGAGACATCATCAAACAGACCACCCACA	720
Db	658	TATGAAACCTACACCAGAGCTTCTTCATAGGAGCATCATCAAACTGACCCACCCCAAG	717
QY	721	AACCTGCGAGTGAAGCCATTGAAAAAATTTCTGGCACGTGGAGCTGACGTGGGATATCCC	780
Db	718	AACCTGCGAGTGAAGCCATTGAAAAAATTTCTGGCACAGTGGAGCTGACGTGGGATATCCC	777
QY	781	GACACCTTGAGACACCCACATTCCTACTTCCTCCCTGACATTTTTCATACAGCCCGAGGC	840
Db	778	GACACCTTGAGTACTCCACATTCCTACTTCCTCCCTGACATTTTTCATACAGCCCGAGGC	837
QY	841	AAGAACATTAGAGAAAAGAAAGATAGACTTGGCTGGACAAAGCTCAGCCAAAGTGGTG	900
Db	838	AAGAACATTAGAGAAAAGAAAGATAGAGTCTTCACGACAAACCTCAGCCAGGTCATC	897
QY	901	TGGCACAAGATATGCCAGAGATCCGGGTGGCAAGCCCGAGCCGCTACTATATGTTCATCTGG	960
Db	898	TGGCACAAGATATGCCAGAGATCCGGGTGGCAAGCCCGCTACTATATGTTCATCTGG	957
QY	961	AGCACTAGGAGATTTGTGTATGACAGTGGTGGCGGT-----	996
Db	958	AGCAATATGAGATTTGTGTATGAGTGGGTGGGTGGCAAGCCGGGTGGCGGAAGCGGC	1017
QY	997	GCGCGCGGATCTAGAAACTTGGCCAAACCCCTACTCATCCCGGGATATGTTCCATGTTTG	1056
Db	1018	GGTGGCGGACAGCAAAACCTCCCTGGGCACTCCAGACCCAGGATGTTCCTCATGCCCTT	1077
QY	1057	AACCACTCCCAAACTTGTGTGAGAGCGGTGACACACCTTCACAAAGCCCGAGCAAACT	1116
Db	1078	CACCACTCCCAAACTGTGTGAGAGCGGTGACACACCTTCACAAAGCCCGAGCAAACT	1137
QY	1117	CTGAAATTTATTTCTCTGACTTCCGAAGAGATTGATCATGAGAGATATCAAAAGATATA	1176
Db	1138	CTGAAATTTTACCTTGTCACTTCTGAAAGAGATTGATCATGAGAGATATCAAAAGATATA	1197
QY	1177	ACCAGACACAGTGGAGGCTGTGATACCATCTGGAATTAAACATGATAGAGTTGCCGTGCT	1236
Db	1198	ACCAGACACAGTGGAGGCTGTGATACCATCTGGAATTAAACATGATAGAGTTGCCGTGCT	1257
QY	1237	TTCGAGACAGATCTCTTTGATTAACCAAGGGAGTGTGCTGGCCCTGGAAAGGCCCTTTT	1296
Db	1238	TTCGAGACAGATCTCTTTGATTAACCAAGGGAGTGTGCTGGCCCTGGAAAGGCCCTTTT	1317
QY	1297	ATGACGGCTGCTGTGCTTACAGCATCTATAGAGACTTCAAGATGTACAGATGGAATTC	1356
Db	1318	ATGATGGGCTGCTGTGCTTACAGATCTTATAGAGACTTCAAGATGTACAGATGGAATTC	1377
QY	1357	AAGGCATGAAAGCGCAAGCTTTTAAATGATCCCAAGAGCAGATCTTCTGGATCAAAAC	1416
Db	1378	AAGGCATGAAAGCGCAAGCTTCTGATGATGATCTTCAAGAGCAGATCTTCTGGATCAAAAC	1437
QY	1417	ATGTCGAGACCTATCGATGAGAGCTTTAAAGAGCCCTGAATTTTCAACAGTGTGCTGGCA	1476
Db	1438	ATGTCGAGACCTATCGATGAGAGCTTTAAAGAGCCCTGAATTTTCAACAGTGTGCTGGCA	1497
QY	1477	CAGCAATCTCTCTTGAAGAGCCGAGATTTTATAAAGCTAAATCAAGCTCGCATACTT	1536
Db	1498	CAGCAATCTCTCTTGAAGAGCCGAGATTTTATAAAGCTAAATCAAGCTCGCATACTT	1557
QY	1537	CTTTCATCTCTTCAAGATTTGCTGGGTGACATCAATAGATGATGTCTTACTTGAATCTT	1596

Db 1558 CTTGATGCTTTGAGAAATTCGGGAGTGAATGACATGTGACAGAGTACAGAGCTATCTGAATGCT 1617
QY 1597 TCC 1599
Db 1618 TCC 1620

RESULT 3
AR091393 6139 bp DNA Linear PAT 07-SEP-2000
LOCUS Sequence 7 from patent US 5994104.
DEFINITION AR091393
ACCESSION AR091393
VERSION AR091393.1 GI:10018148
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 6139)
AUTHORS Anderson, R. James., Prentice, H. Grant. and MacDonald, I. Duncan.
TITLE Interleukin-12 fusion protein
JOURNAL Patent: US 5994104-A 7 30-NOV-1999;
FEATURES
source 1. 6139
BASE COUNT 1552 a 1538 c 1558 g 1491 t
ORIGIN

Query Match 76.3%; Score 1219.4; DB 6; Length 6139;
Best Local Similarity 85.6%; Pred. No. 0;
Matches 1390; Conservative 0; Mismatches 206; Indels 27; Gaps 2;

QY 1 ATGACACCTGACGAGTGGTCACTCTGTTTCCCTGCTTTGCTGGCGCTCCCTC 60
Db 3222 ATGGGTACACGAGTGGTCACTCTGTTTCCCTGCTTTTCCCTGCTTTTCCCTGCTTTCCCTC 3281

QY 61 ATGGCCATATGGGAAGTGGAGAAAGATGTTATGTTAGTGGTGGAGTGGCACCCTAT 120
Db 3282 GTGGCCATATGGGAAGTGGAGAAAGATGTTATGTTAGTGGATGGATGGATCCGGAT 3341

QY 121 GCCCCGAGAAATGGTGGTCTCCTACCTGCCATACCCCTGAAGAAGATGACATCTTGG 180
Db 3342 GCCCTGAGAAATGGTGGTCTCCTACCTGACACCCCTGAAGAAGATGATGACCTGG 3401

QY 181 ACCTCAGCGCAGAGCAGTGAAGTCTAGTGTGTAAGTCTGACCATCCAAATCAA 240
Db 3402 ACCTTGGACCGAGAGAGTGAAGTCTAGTGTGTAAGTCTGCAAAACCTGACCATCCAAATCAA 3461

241 GAATTTGGAGATGCTGGCGCATATACCTGCATTAAGGAGGAGGAGGCTTCTAAGCCATTGC 300
3462 GAGTTTGGAGATGCTGGCGCATATACCTGCATTAAGGAGGAGGAGGCTTCTAAGCCATTGC 3521

QY 301 CTCCTGTTGATTCACAAAAGAGATGATTTGGTCCACTGATATCTTAAGGAGAC 360
Db 3522 CTCCTGCTGCTTCACAAAAGAGATGATTTGGTCCACTGATATTTTAAGGAGAC 3581

QY 361 AAGAATCCAAAATTAAGATCTTTCTGAATGTAGGCAAGAAATTAATTGAGACTTTC 420
Db 3582 AAGAATCCAAAATTAAGATCTTTCTGAATGTAGGCAAGAAATTAATTGAGACTTTC 3641

QY 421 ACATGCTGGTGGTGGAGGCAATCAGTCTGATTTGAATTGAAATCAGTCTCAAAAGTAAGCA 480
Db 3642 ACCTGCTGGTGGTGGAGGCAATCAGTCTGATTTGAAATCAGTCTCAAAAGGAGCA 3701

QY 481 GGGTCTTCTGACCCCAAGGGGTGACATGTGAGCAGTGAACATTTGACGAGAGGGGTG 540
Db 3702 GGGTCTTCTGACCCCAAGGGGTGACATGTGAGCAGTGTCTACACTCTCTGACAGAGAGATC 3761

QY 541 AGAGTGCACAACAGGATTAAGAAGTACACAGTGAAGTCTCAGAGGAGGAGTGCCTGC 600
Db 3762 AGAGGAGACAACAAGAGATTA---GAGTACTCAGTGAAGTCCAGAGGAGACAGTGCCTGC 3818

QY 601 CCGTCTGCCGAGGAGAGCTACCATCGAGTCTGCTGGATGCTATTTCACAGCTCAG 660
Db 601 CCGTCTGCCGAGGAGAGCTACCATCGAGTCTGCTGGATGCTATTTCACAGCTCAG 660

Db 3819 CCAGCTGCTGAGGAGAGTCTGCCATTGAGAGTCAATGTTGATGCCGTTCCACAAAGCTCAAG 3878
QY 661 TATGAAAACCTACACAGCAGCTCTTCATTCAGAGACATCATCAACAGACCAAGCCACCA 720
Db 3879 TATGAAAACCTACACAGCAGCTCTTCATTCAGAGACATCATCAACAGCTGACCCACCA 3938

QY 721 AACCTGCAAGTGAAGCAATTTGAAAATTCGAGCAGCTGAGTGAAGTGGGAATACCC 780
Db 3939 AACCTGCAAGTGAAGCAATTTGAAAATTCGAGCAGCTGAGTGAAGTGGGAATACCC 3998

QY 781 GACACCTGGAGACACCCACATCTCTACTTCTCCCTGACATTTTGCATACAGGCCAGGCC 840
Db 3999 GACACCTGGAGTCTCCACATCTCTACTTCTCCCTGACATTTTGCATACAGGCCAGGCC 4058

QY 841 AAGAACAATAGAGAAAGAAAGATAGACTGCTGCTGACAGACACTCAGACCAAGTGGTG 900
Db 4059 AAGAACAAGAGAGAAAGAAAGATAGACTTCTTCACAGGACAAAGACTCAGACCAAGTGTATC 4118

QY 901 TGCACAAGGATGGCAAGATCCGGGTGCAAGCCGAGACCGCTACTATAGTTCAATCTGG 960
Db 4119 TGCAGCAAAATATGACAGATTAAGCGTGGCGGCGCAGAGACCGCTACTATAGCTCATTTGG 4178

QY 961 AGCCACTGGGATCTGTGTCTATGCAATGTGTGGCGT----- 996
Db 4179 AGCCAAATGGGATCTGTGTCTATGCAATGTGTGGCGTGGAGACCGCGGCGGAGAGCGGC 4238

QY 997 GCGCGCGGATCTGCAAACTTGTCCAAACCCCTACTCCATCCCGGGATGTTTCATGTTTG 1056
Db 4239 GGTGGCGGCAACACAAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4298

QY 1057 AACCACTCCCAAGCTTGTGAGAGCCGTGAGCAACACGCTTCAGAAAGCCAGCAAACT 1116
Db 4299 CACCACCTCCCAAAAGCTGCTGAGAGCCGTGAGCAACACGCTTCAGAAAGCCAGCAAACT 4358

QY 1117 CTGAAATTAATTCCTGACATTCGGAAGAGATTCATCATGTAAGATATCACAAGAGATTA 1176
Db 4359 CTGAAATTAATTCCTGACATTCGGAAGAGATTCATCATGTAAGATATCACAAGAGATTA 4418

QY 1177 ACCAGCAGAGTGAAGGCTGCTTACACACTGGAATTAACATGAATGAGACTTGGCTGCT 1236
Db 4419 ACCAGCAGAGTGAAGGCTGCTTACACACTGGAATTAACATGAATGAGACTTGGCTGCT 4478

QY 1237 TCCAGAGAGATCTCTTGTATTAACAGGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCT 1296
Db 4479 TCCAGAGAGATCTCTTGTATTAACAGGAGTGGCTGCTGCTGCTGCTGCTGCTGCT 4538

QY 1297 ATGACGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1356
Db 4539 ATGATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4598

QY 1357 AAGGCATGAAGGCAAGCTTTTATGATGCCCAAGAGGAGATCTTCTGATCAAAAC 1416
Db 4599 AAGGCATGAAGTGAAGCTTTCTGATGATGCTTAAGAGGAGATCTTCTGATCAAAAC 4658

QY 1417 ATGCTGACAGCTATTCATGATGACCTGTTACAGGCTGTAATTTCAACAGTGTACGTGCA 1476
Db 4659 ATGCTGAGAGTATTAATGATGACCTGATGAGCCCTGGAATTTCAACAGTGTACGTGCA 4718

QY 1477 CAGAAATCTCCCTTGAAGAGCCGGAATTTTATTAACCTAAATCAAGCTGATACTT 1536
Db 4719 CAAAAATCTCCCTTGAAGAGCCGGAATTTTATTAACCTAAATCAAGCTGATACTT 4778

QY 1537 CTTGATGCTTTCAGAAATTCGTGCGGTGACATTCATATGAAGATGATGCTTCTACTTAACCT 1596
Db 4779 CTTGATGCTTTCAGAAATTCGTGCGGTGACATTCATATGAAGATGATGCTTCTACTTAACCT 4838

QY 1597 TCC 1599
Db 4839 TCC 4841

RESULT 4
AR091393

LOCUS AR091395 1560 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 11 from patent US 5954104.
ACCESSION AR091395
VERSION AR091395.1 GI:10018150
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1560)
AUTHORS Anderson, R. James., Prentice, H. Grant, and MacDonald, I. Duncan.
TITLE Interleukin-12 fusion protein
JOURNAL Patent: US 5954104-A 11 30-NOV-1999;
FEATURES
source 1..1560
location/Qualifiers
BASE COUNT 443 a 375 c 393 g 349 t
ORIGIN
Query Match 73.3%; Score 1172.4; DB 6; Length 1560;
Best Local Similarity 85.7%; Pred. No. 0;
Matches 1337: Conservative 0; Mismatches 159; Indels 27; Gaps 2:
QY 64 GCATATGCAAGCTGGAGAAAGATGTTATGTTAGAGTTGGAGCTGCACCGTGATGCC 123
DB 1 GCCATATGCGAAGTGAAGAAAGATGTTATGTTAGATTGATGATGATCCGATGCC 60
QY 124 CCGGAGAAATGCTGCTCTCACCCTGGCATACCCCTGAAGAAGATGACTGCTTGACC 183
DB 61 CCGGAGAAATGCTGCTCTCACCCTGGCATACCCCTGAAGAAGATGATACCTGGACC 120
QY 184 TCAGCGCAGAGAGCTGAAGTGAAGTCTGATTAAGCTGATGACGATGCAGTCAAGAA 243
DB 121 TTGGACACAGCAGTGAAGTCTTACGCTCTGCAAAACCTGATGACCAAGTCAAGAG 180
QY 244 TTGGAGATGCTGGCAGTATACCTGCAATTAAGAGAGGAGCTTGACGGTCACTC 303
DB 181 TTGGAGATGCTGGCAGTATACCTGCAATTAAGAGAGGAGCTTGATCCATTCGCTC 240
QY 304 CTGTTGATTCACAAAAAAGAAAGATGGAATTTGCTGCACCTGATATCTTAAGGAACAGAA 363
DB 241 CTGCTGCTTCACAAAAGAAAGATGGAATTTGCTGCACCTGATATTTTAAGGACCAAGAA 300
QY 364 GAATCAAAAATATAGATCTTTCTGAATATGTGAGGCAAAAGATTTATCTGGAGCTTGACA 423
DB 301 GAAGCCAAAATATAGACCTTTCTTAAGATGCGAGGCAAGAAATTTATCTGGAGCTTGACC 360
QY 424 TCGTGGTGGCTGAGCGGCAATCACTGATTTGAATTCAGTGTGCAAAAAGATGACAGAGCC 483
DB 361 TCGTGGTGGCTGAGCGGCAATCACTGATTTGAATTCAGTGTGCAAAAAGATGACAGAGCC 420
QY 484 TTCTGTGACCCCAAGGGGTGACATGTGGAGAGTGCACCTTTCGAGAGAGGGGTGACA 543
DB 421 TTCTGTGACCCCAAGGGGTGACGTTGGAGAGTGCACCTTTCGAGAGAGGGGTGACA 480
QY 544 GTGACACAGAGGATTTATAGAAATGACAGTGGAGTGTGAGGAGGAGTGTGCTGGCCG 603
DB 481 GGGGCAACACAGAGATAT---GAGTACTGAGTGGAGTGTGAGGAGGAGATGATGCTGGCCA 537
QY 604 TCTGCGGAGAGAGGCTTACCATCGAGGTGCTGGTGGATGCTATTTACAAAGCTCAAGTAT 663
DB 538 GCTGCTGAGAGAACTGCTGCCATTTGAGGTGATGCTGGCTGGCTTACAAAGCTCAAGTAT 597
QY 664 GAAAACTACACAGAGCTTTCTTCATGAGAGATCATCAAAAGCAGACCCACCCCAAGC 723
DB 558 GAAAACTACACAGAGCTTTCTTCATGAGAGATCATCAAAAGCAGACCCACCCCAAGC 657
QY 724 CTGAGAGTGAAGCAATTTGAAAAATTTCTGGGACGTGAGCTGAGTGGGAATTAATCCGAC 783
DB 658 TTGAGAGCTGAAGCAATTTGAAAAATTTCTGGGACGTGAGAGTGGAGTGAAGTGAAGCTTGA 717
QY 784 ACCTGGAGACACCCCAATTCCTACTTCTGCCCTGACATTTTGGCATACAGCCCTGAGGCAAG 843
DB 718 ACCTGGAGAGCTGACATTCCTACTTCTGCCCTGACATTCCTGAGCTGACAGGCAAG 777

QY 844 AACATAGAGAAAGAAAGATAGACTCTGCTGGACAGAGACTCAGCCAAAGTCTGTCG 903
DB 778 ACCAAGAGAGAAAGAAAGATAGAGTCTTTCACAGGACAGAGACTCAGCCAGCTCATCTG 837
QY 904 CACAAGAGATGCCAGATCCGCTGCAAGCCGAGACCGCTACTATAGTTGATCTCGAGAG 963
DB 838 CCAAAAATGCCAGATTAAGCTGCGGGGCCAGAGACCGCTACTATAGCTCATCTTGGAGC 897
QY 964 GACTGGGCAATCTGTCTCATGACAGTGTGGCGGT-----GGC 999
DB 898 GAATGGCATCTGTGCGCTGACAGTGTGGCGGTGAGAGGGGGGTGGGAGCGCGGT 957
QY 1000 GCGGATCTAGAACTTGGCAACCCCTACTGCTATCCCGGGGTATGTTCCATGTTGAAC 1059
DB 958 GCGGATGAGAGAACTCTCCCTGCTGGCTCCAGACAGAGATATGTTCCATGCTTAC 1017
QY 1060 CACTCCCAACCTGTTGAGAGCGCTCCAGACACAGCTTCAGAGGCGCAGACAACTCTA 1119
DB 1018 CACTCCCAACCTGTTGAGAGCGCTCCAGACACAGCTTCAGAGGCGCAGACAACTCTA 1077
QY 1120 GAATTAATCTGCTGACCTTCCAGAGATGATGATGATGATGATGATGATGATGATGAT 1179
DB 1078 GAATTAATCTGCTGACCTTCCAGAGATGATGATGATGATGATGATGATGATGATGAT 1137
QY 1180 AGCAGATGAGAGCTGCTTACCTGATGATGATGATGATGATGATGATGATGATGATGAT 1239
DB 1138 AGCAGATGAGAGCTGCTTACCTGATGATGATGATGATGATGATGATGATGATGATGAT 1197
QY 1240 AGAGAGATCTTGTATTAACCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1299
DB 1138 AGAGAGATCTTGTATTAACCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1257
QY 1300 ACGTCTCTGTGCTTACAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1359
DB 1258 ATGGCTCTGTGCTTACAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1317
QY 1360 GCCATGAAAGCAACCTTTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1415
DB 1318 ACCATGAATGCAAAAGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1377
QY 1420 CTGACAGATGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1479
DB 1378 CTGAGAGATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1437
QY 1480 AATCTCTCTCTTGAAGAGCGGATTTTATAAATAAATAAATAAATAAATAAATAAATAAATA 1539
DB 1438 AATCTCTCTCTTGAAGAGCGGATTTTATAAATAAATAAATAAATAAATAAATAAATAAATA 1497
QY 1540 CATGCTTTCAGAAATTCGCGGTGACCATCAATAGATGATGATGATGATGATGATGATGATGAT 1599
DB 1498 CATGCTTTCAGAAATTCGCGGTGACCATCAATAGATGATGATGATGATGATGATGATGATGAT 1557
RESULT 5
AR151071 990 bp DNA linear PAT 08-AUG-2001
LOCUS AR151071
DEFINITION Sequence 11 from patent US 6231850.
ACCESSION AR151071
VERSION AR151071.1 GI:15117121
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 990)
AUTHORS Okano, F., Satoh, M., and Yamada, K.
TITLE Canine interleukin 12
JOURNAL Patent: US 6231850-A 11 15-MAY-2001;
FEATURES
source 1..990
location/Qualifiers
BASE COUNT 279 a 244 c 249 g 218 t
ORIGIN

Query Match 61.5%: Score 983.8; DB 6; Length 990;
 Best Local Similarity 99.8%: Pred. No. 8.9e-276;
 Matches 985; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 ATGCACCTCAGCAGTGGTCATCTCTGGTTCCTCGTTTTCCTGTTTGTGCGCTCCCTC 60
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Db 1 ATGCATCTCAGCAGTGGTCATCTCTGGTTCCTCGTTTTCCTGTTTGTGCGCTCCCTC 60
QY 61 ATGGCCATATGGGAAGTGGAGAAAGATGTTATGTTGAGAGTTGGACTGGACCCCTGAT 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 ATGGCCATATGGGAAGTGGAGAAAGATGTTATGTTGAGAGTTGGACTGGACCCCTGAT 120
QY 121 GCCCCGGAGAAATGTGTCCTCCTACCTGCCATACCCCTGAAGAAGATGATCATTGG 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 GCCCCGGAGAAATGTGTCCTCCTACCTGCCATACCCCTGAAGAAGATGATCATTGG 180
QY 181 ACCTCAGCGCAGACGACGAGTGAAGTCTTAGGTTCTGGTAAACTCTGACCATCAAGTCAA 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    181 ACCTCAGCGCAGACGACGAGTGAAGTCTTAGGTTCTGGTAAACTCTGACCATCAAGTCAA 240
QY 241 GAATTTGGAGATGCTGGCCATATACCTGCCATAAAGAGGCAAGTTCTGACCGCTCA 300
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    241 GAATTTGGAGATGCTGGCCATATACCTGCCATAAAGAGGCAAGTTCTGACCGCTCA 300
QY 301 CTCTGTTGATTCACAAAAAGAGATGGAATTTGTTCACTGATATCTTAAAGGAACAG 360
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    301 CTCTGTTGATTCACAAAAAGAGATGGAATTTGTTCACTGATATCTTAAAGGAACAG 360
Db 301 CTCTGTTGATTCACAAAAAGAGATGGAATTTGTTCACTGATATCTTAAAGGAACAG 360
QY 361 AAAGAATCCAAAATTAAGATCTTTCTGAAATGTGAGGCAAGAATTAATTCGAGCTTTC 420
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    361 AAAGAATCCAAAATTAAGATCTTTCTGAAATGTGAGGCAAGAATTAATTCGAGCTTTC 420
Db 361 AAAGAATCCAAAATTAAGATCTTTCTGAAATGTGAGGCAAGAATTAATTCGAGCTTTC 420
QY 421 ACATGCTGGTGGCGAGGCGCAATCAGTATGTTGAAATTCAGTGCAAAAGTAAGCAGA 480
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    421 ACATGCTGGTGGCGAGGCGCAATCAGTATGTTGAAATTCAGTGCAAAAGTAAGCAGA 480
Db 421 ACATGCTGGTGGCGAGGCGCAATCAGTATGTTGAAATTCAGTGCAAAAGTAAGCAGA 480
QY 481 GGCCTTCTGACCCCCCAAGGGGTGACATGTGAGACAGTGCACCTTTCAGCAGAGAGGTC 540
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    481 GGCCTTCTGACCCCCCAAGGGGTGACATGTGAGACAGTGCACCTTTCAGCAGAGAGGTC 540
Db 481 GGCCTTCTGACCCCCCAAGGGGTGACATGTGAGACAGTGCACCTTTCAGCAGAGAGGTC 540
QY 541 AGAGTGGACAACAGGAGATTAAAGATACACAGTGCAGAGTGCAGAGGCGCTGC 600
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    541 AGAGTGGACAACAGGAGATTAAAGATACACAGTGCAGAGTGCAGAGGCGCTGC 600
Db 541 AGAGTGGACAACAGGAGATTAAAGATACACAGTGCAGAGTGCAGAGGCGCTGC 600
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QY 841 AAGAACAATAGAGAAAGAAAGATAGACTTGGCGTGGACAAGACCTCAGCCCAAGGCTCTG 900
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QY 961 AGGCACTGGGCACTGTGTCTGAGT 987
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RESULT 6
E15017
LOCUS E15017 990 bp DNA linear PAT 28-JUL-1999
DEFINITION Canine mRNA for interleukin 12 40kDa subunit, complete cds.
ACCESSION E15017
VERSION E15017.1 GI:5709700
KEYWORDS JP 1998036397-A/1.
SOURCE
ORGANISM Canis sp.
  Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
  1 (bases 1 to 990)
REFERENCE
  Okano, F.
  CANINE INTERLEUKIN 12 AND ITS PRODUCTION
  Patent: JP 1998036397-A 1 10-FEB-1998;
  JOURNAL.
  TORAY IND INC
COMMENT
  OS Canis sp. (dog)
  PN JP 1998036397-A/1
  PD 10-FEB-1998
  PF 08-NOV-1996 JP 1996296789
  PR 08-NOV-1995 JP 95P 289729, 23-MAY-1996 JP 96P 128104 PI
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  PC C07K14/54, C07H21/04, C12N5/10, C12N15/09, C12P21/02, (C12N5/10, PC
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RESULT 7
CFU49100 1015 bp mRNA linear MAR 13-MAR-1996
LOCUS
DEFINITION Canis familiaris interleukin-12 p40 subunit mRNA, complete cds.
ACCESSION U49100
VERSION U49100.1 GI:1223907
KEYWORDS
SOURCE
ORGANISM
Canis familiaris.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
AUTHORS Belke-Louis, G.F. and Mueller, M.
TITLE Cloning and sequence analysis of the p35 and p40 subunits of canine interleukin-12
JOURNAL unpublished
2 (bases 1 to 1015)
Belke-Louis, G.F.
Direct Submission
Submitted (13-FEB-1996) Georg F. Belke-Louis, Institute of Med.
Microbiology, Veterinärstr. 13, München, D-80539, Germany
location/qualifiers
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DEFINITION	AR151061	990 bp	DNA
ACCESSION	Sequence 1	from patent US 6231850.	linear
VERSION	AR151061		PAT 08-AUG-2001
KEYWORDS	AR151061.1	GI:15117111	
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 990)		
AUTHORS	Okano, F., Satoh, M. and Yamada, K.		
TITLE	Canine Interleukin 12		
JOURNAL	Patent: US 6231850-A 1 15-MAY-2001;		
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ORIGIN			

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Db	61	ATGGCATATATGGGAAGTGGAGAAAGATGTTATGTGTAGAGTTGGACTGGACCCCTGAT	120
OY	121	GGCCCCGGAGAAATGTGTGTCTCTCACTGGCCATACCCCTGAAGAAGATGACATCACTTGG	180
Db	121	GGCCCCGGAGAAATGTGTGTCTCTCACTGGCCATACCCCTGAAGAAGATGACATCACTTGG	180
OY	181	ACCTCAGCGCGAGAGCAGTGAAGTCCCTAGTGTCTGTAAACCTCAGCATCCAACTGCAAA	240
Db	181	ACCTCAGCGCGAGAGCAGTGAAGTCCCTAGTGTCTGTAAACCTCAGCATCCAACTGCAAA	240
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Db	241	GAATTTGGAGATGCTGGCCAGTATACCTGGCCATAAAGAGCGCAAGTTCTGAGCCGCTCA	300
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OY	361	AAAGAAATCCAAAAATTAAGATCTTCTGAAAATGTGAGCGCAAAAGAAATTAATCTGGACGTTTC	420
Db	361	AAAGAAATCCAAAAATTAAGATCTTCTGAAAATGTGAGCGCAAAAGAAATTAATCTGGACGTTTC	420
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OY	481	GGCTTCTGTGACCCCGAAAGGGGTGACATGTGTGAGAGACGTGACACATTTTCAGACAGAGGGGTC	540
Db	481	GGCTTCTGTGACCCCGAAAGGGGTGACATGTGTGAGAGACGTGACACATTTTCAGACAGAGGGGTC	540
OY	541	AGATGTGACAACAGCAGATTATTAAGAAGTACACAGTGTGATCTCAGAGAGGGGAGTAGTCCCTGCG	600
Db	541	AGATGTGACAACAGCAGATTATTAAGAAGTACACAGTGTGATCTCAGAGAGGGGAGTAGTCCCTGCG	600
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Db	601	CCCTCTGGCGAGGAGAGGCTTACCCATTCGAGTCTGTGGATGTGATTTACAGAGCTCAAG	660
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QY	901	TGCGACAAGGATGCCACAGATCCGCTGGCAAGCCCGACAGCCGCTACTATATAGTTCACTCTGG	960
Db	901	TGCGACAAGGATGCCACAGATCCGCTGGCAAGCCCGACAGCCGCTACTATATAGTTCACTCTGG	960
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RESULT 9	
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AX076200	990 bp
	DNA
	linear
	PAT 06-FEB-2001

Accession	Version	Keywords	Source	Organism	Reference	Authors	Title	Journal
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				artificial sequences.				
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				Lutz,H., Lentemeyer,C., Pedersen,N., Schroff,M. and Wiltig,B.				
				Feline Interleukin-12 as an immune stimulant				
				Patent: WO 0104155-A 1 18-JAN-2001;				
				Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;				
				Universitaet zuerich (CH) ; THE REGENTS OF THE UNIVERSITY OF				
				CALIFORNIA (US)				
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Origin								
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Matches 920;	Conservative 0;	Mismatches 67;	Indels 0;	Gaps 0;				
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DB 1	ATGATCCTCTAGCGAGCTGGTCATCGCCCTGGTTTCCCGCTGGCTGGCACCTCCCTC	60						
QY 61	ATGGCCATATATGAGCAACTGGAGAAGATGTTTATGTTGAGAGTTGGACTGGACCCCTGAT	120						
DB 61	ATGGCCATATGAGCAACTGGAGAAGATGTTTATGTTGAGAGTTGGACTGGACCCCTGAT	120						
QY 121	GCCCGCGGAGAATGGTGGTCTCACCCTGCCATACCCCTGAAGAAGATGACATCACTTGG	180						
DB 121	GCCCGCGGAGAATGGTGGTCTTACCTGCAATACCTCTGAAGAAGATGACATCACTTGG	180						
QY 181	ACCTCAGCGCAGACAGTGAAGTCTCTAGCTTGTGTAAACTCTGACCATCCAACTCAA	240						
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QY 361 AAACATATCAAAAAATATCTTTCTGAAATGTGAGCAAGAAATATATCTGAGCTTC 420
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Db 901 TGCCACAAGGATGCAACATCGCGTGAAGCGTGAAGCGCTACTATAGTTCAATCTGG 960
RESULT 10
AX076482 950 bp DNA linear PAT 05-FEB-2001
LOCUS AX076482
DEFINITION Sequence 8 from Patent WO0104280.
ACCESSION AX076482
VERSION AX076482.1 GI:12711034
KEYWORDS
ORGANISM
SYNTHETIC CONSTRUCT.
artificial construct.
REFERENCE
1 (bases 1 to 950)
AUTHORS Leutenegger, C., Schrott, M., Witzig, B. and Lutz, H.
TITLE Vaccine against lentiviral infections, such as the feline immune
deficiency virus of the cat
PATENT: WO 0104280-A 8 18-JAN-2001
JOURNAL: Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE)
FEATURES
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/organism="synthetic construct"

/db xref="taxon:32630"
/note="Sequence coding for SEQ ID NO 2, IL-12 p40"
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Best Local Similarity 93.2% Pred. No. 2,2e-245;
Matches 920: Conservative 0: Mismatches 67: Indels 0: Gaps 0:
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RESULT 11
LOCUS FCIL12P40 1006 bp mRNA linear MAM 13-MAY-1997
DEFINITION F. catus mRNA for Interleukin-12 p40 chain.
ACCESSION Y07762
VERSION Y07762.1 GI:2102664
KEYWORDS Interleukin-12 p40.
SOURCE cat.
ORGANISM F. catus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.

REFERENCE
AUTHORS Schijns, V.E., Wierda, C.M., Vahlenkamp, T.W. and Horzinek, M.C.
TITLE Molecular cloning of cat Interleukin-12
JOURNAL Immunogenetics 45 (6), 462-463 (1997)
PUBMED 9246745
9089110

REFERENCE
AUTHORS Schijns, V.E.C.J.
TITLE Direct Submission
JOURNAL Submitted (03-SEP-1996) V.E.C.J. Schijns, Virology Division,
Veterinary Faculty Utrecht University, Yalelaan 1, NL-3584 CL
Utrecht, NETHERLANDS

FEATURES
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BASE COUNT 288 a 249 g 211 t
ORIGIN

Query Match 55.0% Score 879.8; DB 4; Length 1006;
Best Local Similarity 93.2% Pred. No. 2.2e-245;
Matches 920; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

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QY 961 AGGACGTGGCATTCTGTGTCATGTCAGT 987
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RESULT 12
LOCUS AX076209 4522 bp DNA linear PAT 06-FEB-2001
DEFINITION Sequence 10 from Patent WO0104155.
ACCESSION AX076209
VERSION AX076209.1 GI:12710834
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequences.
REFERENCE
AUTHORS Lutz, H., Leutenegger, C., Pedersen, N., Schroff, M. and Wiltig, B.
TITLE Feline interleukin-12 as an immune stimulant
JOURNAL Patent: WO 0104155-A 10 18-JAN-2001;
Moligen Fortschungs-, Entwicklung- und Vertriebs GmbH (DE);
Universitaet Zuerich (CH); THE REGENTS OF THE UNIVERSITY OF
CALIFORNIA (US)
location/Qualifiers
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LOCUS	FCU083184	990 bp	MAM 16-JUL-1999
DEFINITION	Felis catus interleukin-12 p40 subunit (IL-12) mRNA, complete cds.		
ACCESSION	U083184		
VERSION	U083184.1		
KEYWORDS	GI:2735050		
SOURCE	Felis catus.		
ORGANISM	Felis catus. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Feliidae; Felis. 1 (bases 1 to 990) Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W., Pedersen,N.C. and Lutz,H. Nucleotide and predicted peptide sequence of feline interleukin-12 (IL-12) JOURNAL DNA Seq. 8 (1-2), 77-82 (1997) MEDLINE 98182592 PUBMED 9522125 2 (bases 1 to 990) Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W., Pedersen,N.C. and Lutz,H. Direct Submission Submitted (24-DEC-1996) Clinical Laboratory, Department of Internal Veterinary Medicine, University of Zurich, Winterthurerstrasse 260, Zurich, 24 8057, Switzerland Location/Qualifiers 1..990 /organism="Felis catus" /db_xref="taxon:9685" 1..990 /note="cytokine" /codon_start=1 /product="interleukin-12 p40 subunit" /protein_id="AAB93835.1" /db_xref="GI:2735051 /translation="MHPQLYIAWFSVLVLAAPLMAIMLEKKNVYVELDWHDPAPGE MVLVLDCTPEDDITWTSDOSEVLGSKITLVKEFADAGQYCHGGEVLHSFPL LHKKEGIMSTDLIRQEKSKNKIFLKCEKNYSGRTGWLTAISIDILKFTVKSRS GSSPDGCVGTGAATLSAEKRYVVDNRDKYVVECOGSAQPAEESIPIEVYNAIHK LKYENYTSFPIRIOLIKPDPKNIQLKPLKRSRVEVSWEPDITWSTHAFSLTFGCV OVQOKNNKEKDRILSVQKTSKVVCHDADAKIRVADRRYYSSSNMAVSACS"		
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Query Match	54.9%	Score 878.2:	DB 4:	Length 990:
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RESULT 15			
LOCUS	AX154603	590 bp	DNA
DEFINITION	Sequence 7 from Patent WO0140257.		
ACCESSION	AX154603		
VERSION	AX154603.1	GI:14516186	
KEYWORDS			
SOURCE	synthetic construct.		
ORGANISM	synthetic construct.		
REFERENCE	artificial sequences.		
AUTHORS	1 (bases 1 to 590)		
TITLE	Leong,S.R. and Punnonen,J.		
JOURNAL	Cytokine polypeptides and nucleic acids		
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	Maxygen, Inc. (US)		
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ORIGIN			

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QY	241	GAATTTGAGAGTGGCTGGCTCAGTATACCTGGCCATAAAGAGAGGCAAGCTTGTGAGCGCTCA	300					
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QY	301	CTCTCTGTTGATTCAACAAAAAGACATGTAATTTGCTCCACTGATATCTTTAAAGAGAC	360					
Db	301	CTCTCTGCTGCTTCACAAAAAGAAATGCAATTTGCTCCACTGATATCTTTAAAGAGAC	360					
QY	361	AAAGAAATTCACAAAATTAACATCTTCTGTGAATGTGAGGGAACAAATTTCTTCGACCTTC	420					
Db	361	AAAGAGGCGCAAAATTAACATCTTCTGTGAATGTGAGGGAACAAATTTCTTCGACGCTTC	420					
QY	421	ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTTGAATTCAGTGTCAAAAGTAGACA	480					
Db	421	ACCTGCTGGTGGCTGACGGCAATCAGTACTGATTTTGAATTCAGTGTCAAAAGTAGACA	480					
QY	481	GAGTCTCTGTGACCCGAGGGGTGAGCTGATGTGAGCAGTGCACATTTTCGACACAGAGGGTC	540					
Db	481	GAGTCTCTGTGACCCGAGGGGTGAGCTGATGTGAGCAGTGTACATCTCTGTGACAGAGGGTC	540					
QY	541	ACAGCTGACACAGCGATTTATAGAAGTACACAGTGGAGTGTTCAGAGAGGCGAGTCCCTGC	600					
Db	541	AGCATGACACACAGCGATTTATAGAAGTACACAGTGGAGTGTTCAGAGAGGCGAGTCCCTGC	600					
QY	601	CGCTCTGTGCGAGGATAGCTACCCATTCGAGGCTCGTGGTGTGATGCTATATTCACAGCTCAAG	660					
Db	601	CGCTCTGTGCGAGGATAGCTATCCCATTCGAGGCTCGTGGTGTGATGCTATATTCACAGCTCAAG	660					

[illegible]

Search completed: January 14, 2003, 23:14:28
Job time : 2908 secs

Canine IL-12 p40
Nucleic acid encode
Nucleic acid encode
Nucleic acid encode
Nucleic acid encode
Nucleic acid encode
Nucleic acid encode
Nucleic acid encode
Nucleic acid encode
Canine coding sequ
Canine full length
Canine mature CLA
Feline IL-12p40
Feline IL-12p40
Feline IL-12p40 e
Feline IL-12p40
Plasmid pmol-fil112
Feline FLAPp40 cDN
Modified human cy
Feline FLAPp40 cDN
Feline FLAPp40 cDN
Feline FLAPp40 cDN
Modified human cy
Modified human cy
Human p40-IL-2 coo
Human Interleukin
Human Interleukin
DNA encoding huma
Human interleukin
Human cytokine p40
human interleukin
EPV 42 kb promote
EPV 42 kb/human
40 kDa subunit of
40 kDa subunit of
40 kDa subunit of
40 kDa subunit of
Cytotoxic lymphoc
Human p40 coding s
Natural killer cel
Human interleukin

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PD		
XX		10-APR-2001; 2001US-0828825.
PR		27-JUL-2000; 2000KR-0043498.
PA		(LEES/) LEE S.
PA		(KIMH.) KIM H.
PI		Lee S, Kim H;
DR		WP1: 2002-239247/29. P-PSDB; AAEI9820.
PT		New expression system, useful as vaccine for treating cancer, comprises DNA molecule encoding interleukin-12 and costimulatory molecule, operably linked to promoter that directs the expression of DNA molecule
PT		-
XX		Example 1; page 31-36; 76pp; English.
XX		The invention relates to an expression system which comprises a DNA molecule encoding interleukin (IL)-12 and a costimulatory molecule, operably linked to a promoter that directs the expression of the DNA molecule. Expression vectors of the invention are useful for in vitro generation of genetically modified human cancer cells for cancer therapy. These cells share phenotypes of both antigen presenting cells and cancer cells and are suitable as a cellular vaccine for certain types of cancer. Expression vectors are useful for eliciting an anti tumour immune response in a individual. They are useful for activating T cells for immunotherapeutic responses against primary or metastatic cancers. The present sequence is PIRKS-hB7-1-IL12.2 vector DNA. This vector comprises cytomegalovirus (CMV) promoter and enhancer, bacteriophage T7 RNA polymerase promoter, human B7-1 DNA, IRES sequence, human IL-12.2 DNA, bacteriophage T3 RNA polymerase promoter, Simian virus 40 (SV40) fragment containing polyadenylation signal, fl origin of replication, Neo r expression cassette and ampicillin resistance sequence.

XX	Sequence	8608 BP, 2180 A : 2126 C : 2138 G : 2164 T : 0 other:
SQL	Query Match	77.0%: Score 1231.6; DB 24; Length 8608:
	Best Local Similarity	86.2%: Pred. No. 0;
	Matches 1392: Conservative	0: Mismatches 204; Indels 18; Gaps 2:
OY	1 ATGCACCTTCAGACAGTGTGGTCTATCTCTCTGCTTTTCCCTCTGCTTCTGCGCGCTCTCCCTC	60
Db	2640 ATGTGTCTACACACACATGTGTGTCTCTCTGCTTTTCCCTGCTTCTGCGCATCTCCCTC	2699
OY	61 ATGGCATATATGGAACTGTGAGAAAGATGTATTATGTGTAGATGTTGACGTGGCAGCCCTCAT	120
Db	2700 GTGGCATATATGGAACTGTGAGAAAGATGTATTATGTGTAGATGTTGACGTGGCAGCCCTCAT	2759
OY	121 GCCCCCGAGAAATGGTGTCTCCACCTGCATACCCCTGAAGAAGATGACATCTTTG	180
Db	2760 GCCCTGTGAGAAATGGTGTCTCCACCTGTGACACCCCTGAAGAAGATGATATCCTG	2819
OY	181 ACCTCAGCGCAGAGAGATGGAATCCTACGTTCTGTAAACTCTGCACCATCCAAATCAA	240
Db	2820 ACCTTGTGACCGAGAGATGAGTCTTTAGGCTCTGTGCAAAAACCTGTGACATCCAAATCAA	2879
OY	241 GAATTTGAGATATGCTGCGCAGTATACCTGCCATAAGGAGCGCAAGTTCTGAGCGCTCA	300
Db	2880 GAGTTTGGAGATATGCTGCGCAGTATACCTGCCATAAGGAGCGGAGTTCTTAAGCATTCG	2939
OY	301 CTCCTGTTGATTTCACAAAAAGAGATGGAAATTTGTCCACTGATATCTTAAAGSACAG	360
Db	2940 CTCCTGCTGCTTCACAAAAAGAGATGGAAATTTGTCCACTGATATCTTAAAGSACAG	2999
OY	361 AAAGATATCAAAAATTAAGATCTTTCTGAAATGTGAGCAAAAGAAATTTATTCGAGCGTTTC	420
Db	3000 AAAGAACCCAAAATTAAGATCTTTCTGAAATGTGAGCAAAAGAAATTTATTCGAGCGTTTC	3059
OY	421 ACATCTGCTGTGCTGAGCGCATCTGATCTGATTTGAAATTCAGTGTCAAAAGTAGACAGA	480
Db	3060 ACCTGCTGTGTGGCTGACACATCATCTGATTTGATTCAGTGTCAAAAGTAGACAGA	3119
OY	481 GAGCTTCTGACCCCCCAAGGGGTGACATGTGGAGACAGTTCAGCCAGAGAGGCTC	540
Db	3120 GAGCTTCTGACCCCCCAAGGGGTGACATGTGGAGAGTGTGCTACACTCTCTGCGAGAGAGTTC	3179
OY	541 AGAGTGCACAACGAGGATTTATAGAAAGTACACAGTGAAGTGTCAAGAGGAGGAGTCCCTGC	600
Db	3180 AGAGGAGGACAAACAGAGAGTAT--GAGTACACAGTGTGAGGAGGAGGAGGAGTCCCTGC	3236
OY	601 CCGCTGTGCGAGGAGAGCTACCATGCAAGGTCGTGTGTGATGCTATTTCACAAAGTCAAG	660
Db	3237 CCAAGTGTGTGAGGAGAGTGTGCTCCATTAAGGTCAATGAGTGTGAGTCCGTTTCACAAAGTCAAG	3296
OY	661 TATGAAACCTACACAGCAGCTTCTTCATTCAGAGACATCATCAAAACAGACCACCCACA	720
Db	3297 TATGAAACCTACACAGCAGCTTCTTCATTCAGAGACATCATCAAAACCTGACCACCCACAC	3356
OY	721 AACCTGCAGCTGAAGCCATTGAAAAATTTCTGGCAGCTGAGAGTCACTGAGGAAATACCCC	780
Db	3357 AACCTGCAGCTGAAGCCATTGAAAAATTTCTGGCAGCTGAGAGTCACTGAGGAGAGTACCT	3416
OY	781 GACACCTGAGACACCCCATTTCTCAATTTCTCCCTGCAATTTTGATCAAGGCCAGAGGC	840
Db	3417 GACACCTGAGACTCTCCCATTTCTCAATTTCTCCCTGCAATTTCTGAGTTCAAGGTCCAGGGC	3476
OY	841 AAGAACATAGAGAAAAAGAAAGATAGACTCTGCTGTGACAAGACTCAGCCAAAGTCTGTG	900
Db	3477 AAGAGCAGAGAGAAAAAGAAAGATAGACTCTTCACACGACCAAGACTCAGCCAAAGTCTATC	3536
OY	901 TGCACACAGGATGCCAGATTCGGGTGTGAACCCGAGACCCGCTACTATAGTTTCACTCGG	960
Db	3537 TGCACCAAAAATATGCACAGATTAGCTGTGGGCCCCAGGACCGCTACTATAGTTTCACTCTGG	3596
OY	961 AGCGACTGGGCAATCTGTGTCAATGCAAGTGTGGCGGTGCGGCGG-----A	1005

PS Example; Fig 11; 73pp; English.

This sequence encodes the human interleukin-12 fusion protein sequence, designated Flex-12. The invention relates to an isolated nucleic acid construct (1) comprising a region encoding an interleukin-12 (IL-12) fusion protein (comprising an IL-12 p35 subunit, an IL-12 p40 subunit and a linker peptide (joining the subunits)) and a region encoding a B7 protein. (1) may be used to produce IL-12 fusion proteins according to standard recombinant DNA methodologies. The fusion proteins may be produced either *in vitro* in a fermentation culture or *in vivo* as part of a gene therapy protocol (in this case (1) is used to transform a patient's cells, which then secrete the functional polypeptide to supplement the patient's own production of IL-12 or to rectify mutations which lead to the expression of inactive polypeptides). The fusion proteins produced in this way may be used to treat any disease which responds to IL-12 such as tumours (both solid and dispersed of the kidney, breast, colon, ovarian and cervical tumours and melanomas) and in particular, tumours of the blood such as leukaemia. Alternatively, the polypeptides may be used as antigens in the production of antibodies to IL-12 and to assay for agonists and antagonists of its activity. The antibodies and antagonists may be used to inhibit the activity of IL-12. (1) may also be used diagnostically as a probe which hybridizes to sequences encoding IL-12 and the antibodies may be used to detect the presence of IL-12 polypeptides in samples. They may be used diagnostically to quantitate the expression of the polypeptide by patients and hence which subjects may be in need of restorative therapy.

50 Sequence 6135 BP; 1552 A; 1538 C; 1558 G; 1491 T; 0 other;

Query Match 76.38; Score 1219.4; DB 21; Length 6139;

Matches 1390; Conservative 0; Mismatches 206; Indels 27; Gaps 2;

[illegible]

QY	601	CCCTCTCTCCGAGGAGACCTTACCCATTCGAGGTCGTGTGTGGATGCTATTTCACAAGCTCAAG	660
Dp	3819	CCACCTCTCTGAGGAGGAGTCTTCCCTTTCGAGGTCATGTGTGTGATGCGCTTCACAAAGCTCAAG	3878
QY	661	TATGAAAACCTACACACACACCTCTTTCCTATCAGAGACATCATCAAAACCGAGCCACCCCA	720
Dp	3879	TATGAAAACCTACACACACACCTCTTTCCTATCAGAGACATCATCAAAACCTGACCCACCCCAAG	3928
QY	721	AACCTGACAGCTGAAGGCCATTGAAAAAATCTCGGCACGTCGAGAGTCAAGCTGGGAATACCCC	780
Dp	3939	AACCTGACAGCTGAAGGCCATTGAAAAAATCTCGGCACGTCGAGAGTCAAGCTGGGAATACCCC	3998
QY	781	GACACCTGAGAGACCCCACTTCCCTACTTCTCGCTGACATTTTGGATACAGGCCAGGGC	840
Dp	3999	GACACCTGAGAGTACTCCACATTTCTACTTCTCCCTGACATTTCTGGTTAGAGTCCAGGGC	4058
QY	841	AAGAACAAATAGAGAAAAAGAAAGATATACACTCTGCTGGACACAGACCTCAGCCAGAGTCGTG	900
Dp	4059	AAGAGCAAGAGAGAAAAAGAAAGATATAGAGTCTTTCAGCGACACAGACCTCAGCCAGCTATC	4118
QY	901	TGCCACACAGATGCGCAAGATCCGCTGTGCAAGCCCGAGACCGCTACTATATGTTTCATCTGG	960
Dp	4119	TGCCCCCAAAATGCGCACATTTACCGTCGCGGGCCCAAGACCGCTACTATAGCTCATCTTGG	4178
QY	961	AGTCACCTGGGCACTCTGTGTATGCTACCTGGTGGGGCGT-----	996
Dp	4179	AGTCAAATGGCATCTCTGTGCTCTCACTGCTGAGCGGGTGGAGAGCGCGGTGGCGGAACGCCC	4238
QY	997	GCGCGCGGATCTAGAAAATTGGCCCAACCCCTACTCCATCCCGCGGTATGTTCGAATGTTTG	1056
Dp	4239	GGTGGCGCGAGCGAAAAACCTCCCTCGGCGCATCCAGACCCAGAAATGTTCCCATGCTTT	4298
QY	1057	AAGCAGCTCCCAAACTGTTGGTAGAGCGCTGACCAACACGCTTCACAAGGCCAGACAACCT	1116
Dp	4299	CAGCAGCTCCCAAACTGCTGAGAGCGCGTGCAGCAATCTCTCAACAAGGCCAGACAACCT	4358
QY	1117	CTGAAATTTATTTCTCTGCACTTTCGGAAGAGATTGATCATGAAGATATACAAAGATTAA	1176
Dp	4359	CTGAATTTTACCCTTGGCACTTCTGGAAGAGATTGATCATGAAGATATACAAAAGATTAA	4418
QY	1177	ACGAGCACAGTGAAGGCCCTGCTTACCATCTGGAATTTAACCATGATGAAGATTGCCGTCT	1236
Dp	4419	ACGAGCACAGATGAGGCGCTGTTTACCATTGGAAATTAACCAAAATGAGAGTTGCCCTAAAT	4478
QY	1237	TCCGAGAGATCTCTTTGATTAACCTACAGGAGATGCGTGGCTCTGGAAGAGCCCTCTTT	1296
Dp	4479	TCCGAGAGAGACCTCTTTCAATAACTATATGGAGTTGCTGTGCCCTCCAGAAAGACCTCTTT	4538
QY	1297	ATGACGCTCTGTGCTTTCAGACACATCTATGAGAGCTTGAAGATGTACCAATGGAATTC	1356
Dp	4539	ATGATGGCCCTGTGCTTTCAGTACTATTTATGAAGACTTGAAGATGTACCAAGTGGAGTTTC	4598
QY	1357	AAGGCCCTGAGAGCAAAAGCTTTTAAATGATGATCCAGAGGACAGATTTCTGGATTCAAAAC	1416
Dp	4599	AAGGCCCTGAGATCAAAAGCTTTTCATGATGATCTTAAGAGGACAGATTTCTTGTAGATCAAAAC	4658
QY	1417	ATGCTGACAGCTATGATGAGCTGTATACAGGCCCTGAAATTTCAACAGTGTACTGTGCA	1476
Dp	4719	CAAAAATCTCTCCCTTGAAGAAGCGGATTTTATATAAATCAAAATCAACCTCTGATACTT	4778
QY	1537	CTTCATCTCTTTCAGAAATTTGCTGGCGAGACATCAATATGATGATGTCTCTTCAATCAACT	1596
Dp	4779	CTTCATCTCTTTCAGAAATTTGCTGGCGAGTACTATTGACAGAGTGTACAGAGCTATCTGATGCT	4838
QY	1597	TCC 1599	
Dp	4839	TCC 4841	

ID	Location/Qualifiers
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ID	AADJ31545 standard; DNA; 8578 BP.
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AC	AADJ31545;
XX	
DT	18-JUN-2002 (first entry)
XX	
DE	pIRES-hb7-1-IL12.1 vector DNA.
XX	
KW	Expression system; interleukin-12; cancer therapy; cellular vaccine; immunotherapeutic response; IL-12.1; chimeric; human; Simian virus 40; SV40; cytomegalovirus; CMV; ds.
OS	Chimeric - Cytomegalovirus.
OS	Chimeric - Bacteriophage T7.
OS	Chimeric - Homo sapiens.
OS	Chimeric - Bacteriophage T3.
OS	Chimeric - Rhesus macaque polyoma virus.
XX	Chimeric - Unidentified.
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FT	promoter
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FT	promoter
FT	/note= "T3 RNA polymerase promoter"
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FT	misc_feature
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FT	misc_feature
FT	ampicillin resistance
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PN	US2002018767-A1.
XX	
PD	14-FEB-2002.
XX	
PP	10-APR-2001; 2001US-0828825.
XX	
PR	27-JUL-2000; 2000KR-0043498.
XX	

PA	(LEES/J)	JEE S.
PA	(KIM/H)	KIM H.
XX		
P1	Lee S,	Kim H;
XX		
DR	WP1: 2002-239247/29.	
XX	P-PSDB: AAE19817.	
PT	New expression system, useful as vaccine for treating cancer, comprises DNA molecule encoding Interleukin-12 and costimulatory molecule,	
PT	operably linked to promoter that directs the expression of DNA molecule	
PS	Example 1: page 10-15; 76pp; English.	
CC	The invention relates to an expression system which comprises a DNA	
CC	molecule encoding interleukin (IL)-12 and a costimulatory molecule,	
CC	operably linked to a promoter that directs the expression of the DNA	
CC	molecule. Expression vectors of the invention are useful for in vitro	
CC	generation of genetically modified human cancer cells for cancer	
CC	therapy. These cells share phenotypes of both antigen presenting cells	
CC	and cancer cells and are suitable as a cellular vaccine for certain	
CC	types of cancer. Expression vectors are useful for eliciting an anti-	
CC	tumour immune response in a individual. They are useful for activating	
CC	T cells for immunotherapeutic responses against primary or metastatic	
CC	cancers. The present sequence is P1BES-B87-1-IL12.1 vector DNA.	
CC	This vector comprises cytomegalovirus (CMV) IE promoter and enhancer,	
CC	bacteriophage T7 RNA promoter, human B7-1 DNA, IRES sequence, human	
CC	IL-12.1 DNA, bacteriophage T3 RNA polymerase promoter, Simian virus 40	
CC	(SV40) fragment containing polyadenylation signal, [I] origin of	
CC	replication, Neo r expression cassette and ampicillin resistance	
CC	sequence.	
SQ	Sequence 8578 BP; 2176 A; 2122 C; 2120 G; 2160 T; 0 other:	
Query Match	76.1% Score 1216.6; DB 24; Length 8578:	
Best Local Similarity	86.1%; Pred. No. 0;	
Matches 1377; Conservative	0; Mismatches 204; Indels 18; Gaps	
OY	1 ATGCACCCCTCAGCGAGTTGGTTCATCTCCCTGTTTTCCCTGTGGCGCTCCCTC 60	
DB	2640 ATGTGTCAACGACGAGTTGGTTCATCTCTTGTTGCCGTGTTTCTTGCGATCTCCCTC 2699	
OY	61 ATGSCCATATGGGAATCTGGAGAAGAAGATTATGTTTAGAGCTTGGACTGCCACCCTGAT 120	
DB	2700 GTGGCCATATGGGAACCTGAAGAAAGATTATATGCTGAAGTAATGGATTGGTATCCGAT 2759	
OY	121 GCCCGCGAAGAAATGGTGTCTCCACCTGCCATACCCCGAAGAAAGATGACATCACTTGG 180	
DB	2760 GCCCCTGGAGAAATGGTGTCTCCACCTGTGACACCCCTGAAGAAAGATGTATCACTTGG 2819	
OY	181 ACCTCAGCGCGAGACAGTGAAGTCTTACGTTCTGGTAAACCTTGACCATCCAACTCAA 240	
DB	2820 ACCTTTGGACACGAGACAGTGAAGTCTTACGTTCTGGCAAAACCTTGACCATCCAACTCAA 2879	
OY	241 GAATTTGGAGATGCTGGCCAGTATACCTGCGCATAAAGSAGSGCAAGTTCGTGACCGCTCA 300	
DB	2880 GAGTTTGGAGATGCTGGCCAGTATACCTGCGCATCAAAAGSAGSGGAGTTCGTAAAGCATTCG 2939	
OY	301 CTTCCTGTGATTTCACAATAAAGAAAGATGGATTGGTCCACAGATATCTTAAAGSAGACAG 360	
DB	2940 CTCCTGTGCTTTCACAATAAAGSAGATGGAAATTTGTCCTACATGATATTTTAAAGSAGCACG 2999	
OY	361 AAAGAATTCAAAATAATAGATCTTCTGTGAATGTGAGCGCAAGAATTAATTTCTGACGTTTC 420	
DB	3000 AAAAGAACCCAAAATAATAGACCTTTCTTAAGATGCGCGCAAGAATTAATTTCTGACGTTTC 3059	
OY	421 ACAATGCTGTGGCGAGCGCAATCAGTCTGATTTGGAATTCAGTGTCAAAAAAGTAGCGAGA 480	
DB	3060 ACCTGCTGTGTGGCGAGCGCAATCAGTCTGATTTGGAATTCAGTGTCAAAAAAGCGAGAGA 3119	
OY	481 GGCTTCTCTGACCCCAGGCGGTGACATGTGAGACATGACACTTTCAGCAGAGAGGGTTC 540	


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Db 4182 GTGACTATTGATGAGTATGAGCTATCTGAACTGCTTC 4220

RESULT 6
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ID AAD31547 standard; DNA: 8623 BP.
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XX AAD31547;
AC
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XX 18-JUN-2002 (first entry)
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DE pIRES-hb7-1-IL12.3 vector DNA.
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XX Expression system: interleukin-12; cancer therapy; cellular vaccine;
KW immunotherapeutic response; IL-12.3; chimeric; human; Simian virus 40;
KM SV40; cytomegalovirus; CMV; ds.
XX
XX Chimeric - Cytomegalovirus.
OS Chimeric - Bacteriophage T7.
OS Chimeric - Homo sapiens.
OS Chimeric - Bacteriophage T3.
OS Chimeric - Rhesus macaque polyoma virus.
XX Chimeric - Unidentified.
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XX (KIMH/) KIM H.
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XX Lee S, Kim H;
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XX WPI: 2002-239247/29.
XX P-PSDB: AAE19819.
XX
XX New expression system, useful as vaccine for treating cancer, comprises
XX DNA molecule encoding interleukin-12 and costimulatory molecule,
XX operably linked to promoter that directs the expression of DNA molecule
XX
XX Example 1; Page 24-29; 76pp; English.
XX
XX The invention relates to an expression system which comprises a DNA
XX molecule encoding interleukin (IL)-12 and a costimulatory molecule,
XX operably linked to a promoter that directs the expression of the DNA
XX molecule. Expression vectors of the invention are useful for in vitro
XX generation of genetically modified human cancer cells for cancer
XX therapy. These cells share phenotypes of both antigen presenting cells
XX and cancer cells and are suitable as a cellular vaccine for certain
XX types of cancer. Expression vectors are useful for eliciting an anti
XX tumour immune response in a individual. They are useful for activating
XX T cells for immunotherapeutic responses against primary or metastatic
XX cancers. The present sequence is pIRES-hb7-1-IL12.3 vector DNA.
XX This vector comprises cytomegalovirus (CMV) promoter and enhancer,
XX bacteriophage T7 RNA polymerase promoter, human B7-1 DNA, IRES sequence,
XX human IL-12.3 DNA, bacteriophage T3 RNA polymerase promoter,
XX simian virus 40 (SV40) fragment containing polyadenylation signal, f1
XX origin of replication, Neo r expression cassette and ampicillin
XX resistance sequence.
XX
XX Sequence 8623 BP; 2182 A; 2128 C; 2147 G; 2166 T; 0 other;
SQ
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XX Query Match 76.1%; Score 1216.6; DB 24; Length 8623;
XX Best Local Similarity 85.5%; Pred. No. 0;
XX Matches 1392; Conservative 0; Mismatches 204; Indels 33; Gaps 2;
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QY 1 ATGCACCCCTCAGCAGTTGGTCATCTCCTGTTTCCCTGTTTGCCTGCCCTCCCTC 60
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Db 2640 ATGTGTCACCCAGCAGTGGTCATCTCCTGTTTCCCTGTTTGCCTGCCCTCCCTC 2699
QY 61 ATGGCCATATGGGAAGTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACTGAT 120
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Db 2700 GTGGCCATATGGGAAGTGGAGAAAGATGTTTATGTTGTAGAGTTGGATGATCCGAT 2759
QY 121 GCCCCGCGAAGATGGTGGTCCCTCACCTCCATACCCCTGGAAGGAAGATGATCACTTGG 180
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Db 2760 GCCCCTGGAGAAATGGTGGTCCCTCACCTCCATACCCCTGGAAGGAAGATGATCACTTGG 2819
QY 181 ACCTCAGCGCAGAGCAGTGAAGTCTAGGTTCTGTGTAACCTGATCCATCCCAAGTCAAA 240
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Db 2820 ACCCTGGACACAGCAGTGAGTCTTAGGCTCTGGCAAAACCTGACCATCCAGTCAAA 2879
QY 241 GAATTTGGAGAGTGGCGCAGTATACCTGCGATTAAGAGAGCAAGTTGTGAGCCGCTCA 300
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QY 301 CTCCTGTTGATTCACAAAAGAGATGGAATTTGTCACATGATATCTTAAGAGACAG 360
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2940 CTCCTGCTCTTCACAAAAGAGATGGAATTTGTCACATGATATTTTAAGAGACAG 2999
QY 361 AAAGAAATCCAAAATTAAGATCTTTCTGAATCTGAGGCAAGAAATTTATCTGAGACTTTC 420
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3000 AAAGAAATCCAAAATTAAGATCTTTCTGAATCTGAGGCAAGAAATTTATCTGAGACTTTC 3059
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OY	423	ACGGCTGGGCGTGCAGCGCAATTCAGTACTGATTGTAATTCAGTGTCAAAGTCCAGACA	480
Db	3060	ACCTGCTGGTGGCTGCAGCAATACTGACTGATTGTACATTAGTGTCAAAGCAGCACGA	3119
OY	481	GCGTTCTCTGACCCTCCCAAGGGGTGACATGTGGAGCATGTCACACTTTCACACAGAGGGT	540
Db	3120	GGCTCTTCTGACCCCCCAAGGGGTGACGTGGGAGCTGTCTACACTCTCTGCACAGAGAGTC	3179
OY	541	AGAGTGCACACAGGAGTATTAAAGAATCACAGTGGAGTGTACAGAGGGCAGTGGC	600
Db	3180	AGAGGGGACAACAAGGGAGTAT---GAGTACTCTAGTGGATGCCAGAGAGCAGTGGCTGC	3238
OY	601	CCCTCTGGCCAGGAGGACCTCAACCATTCGAGGTCTGGTGGTAGATGTATTCACAGCTCAG	660
Db	3237	CCAGCTCTCTAGGAGTCTGCCCTATTGGATGGATGGTGGATGGCTGTCCACAAAGTCCAG	3298
OY	661	TATGAAAACATACACACGACACTTCTTCATCAGAGCATCATCAACACAGACCACCCACA	720
Db	3297	TATGAAAACATACACACGACACTTCTTCATCAGGACATCATCAACCTGACCCACCCAAC	3356
OY	721	AACCTCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAAGTGGGAATACCCC	780
Db	3357	AACCTCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAAGTGGGAATACCC	3418
OY	781	GACACCTGGGAGACACCCCAACTCTCTACTCTCTCCCTGACATTTTGGCATACAGGCCAGGGC	840
Db	3417	GACACCTGGGAGTACTCCCAATTCCTCTCTCTCTCCCTGACATTTCTGGCGTTCAAGTCCAGGGC	3478
OY	841	AAGAACATATAGAGAAAAGAAAGATATACACTGTGCTGGAGCAACAGCCAGCAAGSTCTG	900
Db	3477	AAGAGCAAGAGAGAAAAGAAAGATATACAGTCTTCACCGCAACAGACCTCAGCCAGSGTATC	3538
OY	901	TGCCACAAGATGCCAAGATCCGCGGTGCAAGCCCGAGCCGCTACTATATAGTTCAATCTGG	960
Db	3537	TGCCGCAAAAATGTGCACGATTTACGTCGGCGGCCCAAGACCGCTACTATATAGTCAATCTGG	3598
OY	961	AGGCACATGGGCATCTGTGTATGTCAGTGTGGTGGGGTGGGGGG-----	1004
Db	3597	AGCCAAATGGGCATCTGTGCCCTCTCAAGTGTGGGGGTGGAAAGCGTGGCGTGGAAAGCGGT	3656
OY	1005	-----AATTAGAACTTGGCCAAACCCCTTACCCACCTCCACCCCGGGTATGTGTCCA	1050
Db	3657	GGCGGTGGAAAGCCATGAGAGAAACCTCCCGCTGGCCACTTCCAGACCCAGAAATTTGCCA	3716
OY	1051	TGTTTGAACGACTCCCAAACTTGTGAGAGCGCGTCAGCAACACGCTTCAAGAGCCAGA	1110
Db	3717	TGCCCTCACCACCTCCCAAACTGCTGAGGGCGGTGAGCAACATGTCCTCAGAAAGCCAGA	3776
OY	1111	CAAACTCTAGAAATATATTTCTCTGCACTTCCGAAAGATTTGATCATGASAGATATCCAAAG	1170
Db	3777	CAAACTCTAGAAATTTTAAACCTTCCACCTCTGAAAGATTTGATCATGAAATATCCAAAA	3836
OY	1171	GATGAAACCGACAGAGTGGAGGCGCTCTTACCACTGGAAATTAACCATGATGAGAGTTGC	1230
Db	3837	GATGAAACCGACAGAGTGGAGGCGCTTTRACCATTTGGAATTAACCAAGATGAGAGTTGC	3896
OY	1231	CTGGCTTCAGAGAGATCTTGTGATTAACACGGAGTTGGCTGGCTCTGGAAAGGCC	1290
Db	3897	CTAATATTCAGAGAGACTCTTTTCATTAACHAATGGAGTTGGCTGGCTCCAGANAAGCC	3956
OY	1291	TCTTTTATGACGCTCGTGTCTTACGACATCTATGAGAGCTTGAAGATGTACAGATG	1350
Db	3957	TCTTTTATGATGGCCCTGTGGCTTATGATATTTATGAAGACTTGAAGATGTACAGAGTG	4016
OY	1351	GAATTCAGGCCATGAAAGCGAATTTAATGGATCCCAAGGACAGTCTTCTGTGAT	1410
Db	4017	GAGTTCAAGCCATGAAATGGAAGCTTCTGATGATCTTAAAGGACAGTCTTCTTATAT	4076
OY	1411	CAAAACATGCTGACAGTATCGATGAGCTGTTCACAGGCCCTGAATTTCAACAGTGTGACT	1470
Db	4077	CAAAACATGCTGGCAGTATTTGATGAGCTGTATGACAGGCCCTGAATTTCAACAGTGTGACT	4136
OY	1471	GTGCGCAGAAATCTCCCTTGAAGAGCGGATTTTTTATTAATAACTAAATCAAGCTGTGC	1530

Db	Accession	Length	Quality	Sequence	Annotations
Db	4137	GTGCCACAAAAATCTCCCTTGAAGACCGGATTTTATAACTATAAATCAAGCTCTGC	4196		
QY	1531	ATATCTTCTTCATGCTTTTCAGAAATTCGTGCGGTGACCATCATCAATGAATGATGCTCACTTG	1590		
Db	4197	ATACTTCTTCATGCTTTGAGAAATTCGGGCACTGACTATGTGATACAGTAGAGGTATCTG	4256		
QY	1591	AACGCTTCC	1599		
Db	4257	AATGCTTCC	4265		
RESULT 7					
AAD31551	ID	AAD31551	standard; DNA; 8644 BP.		
XX	AC	AAD31551;			
XX	DT	18-JUN-2002	(first entry)		
XX	DE	PIRES-IL12.3-hb7-1 vector DNA.			
XX	OS	Expression system; interleukin-12; cancer therapy; cellular vaccine;			
XX	OS	immunotherapeutic response; IL-12.3; chimeric; human; Simian virus 40;			
XX	OS	SV40; cytomegalovirus; CMV; ds.			
OS	Chimeric - Cytomegalovirus.				
OS	Chimeric - Bacteriophage T7.				
OS	Chimeric - Homo sapiens.				
OS	Chimeric - Bacteriophage T3.				
OS	Chimeric - Rhesus macaque polyoma virus.				
OS	Chimeric - Unidentified.				
XX	Key	Location/Qualifiers			
PH	enhancer	1..750			
FT		/*tag= a			
FT		/note= "CMV enhancer; Also serves as a promoter"			
FT	promoter	1067..1085			
FT		/*tag= b			
FT		/note= "T7 RNA polymerase promoter"			
FT	misc_feature	1090..2731			
FT		/*tag= c			
FT		/note= "Human IL-12.3 DNA"			
FT	CDS	1103..2731			
FT		/*tag= d			
FT		/product= "Human IL-12.3 protein"			
FT	misc_feature	2087..2131			
FT		/*tag= e			
FT		/note= "Linker of human IL-12.3 sequence"			
FT	RBS	2767..3347			
FT		/*tag= f			
FT		/note= "IRES sequence"			
FT	misc_feature	3384..4278			
FT		/*tag= g			
FT		/note= "Human B7-1 DNA"			
FT	promoter	4398..4419			
FT		/*tag= h			
FT		/note= "T3 RNA polymerase promoter"			
FT	polyA_signal	4429..4650			
FT		/*tag= i			
FT		/note= "SV40 fragment containing polyadenylation signal"			
FT	rep_origin	4745..5200			
FT		/*tag= j			
FT		/note= "fl origin of replication"			
FT	misc_feature	5264..5681			
FT		/*tag= k			
FT		/note= "Neo r expression cassette"			
FT	misc_feature	7042..7902			
FT		/*tag= l			
FT		/note= "Ampicillin resistance"			
XX	PN	US2002018767-A1.			

PD 14-FEB-2002.
 XX
 PF 10-APR-2001: 2001US-0828825.
 XX
 PR 27-JUL-2000: 2000KR-0043498.
 XX
 PA (LEES/) LEE S.
 PA (KIM/) KIM H.
 XX
 PI Lee S, Kim H;
 DR WPI: 2002-239247/29.
 DR P-PSDB: AAE19823.
 XX
 PT New expression system, useful as vaccine for treating cancer, comprises
 PT DNA molecule encoding Interleukin-12 and costimulatory molecule,
 PT operably linked to promoter that directs the expression of DNA molecule
 PS
 PS Example 1: Page 52-57; 76pp: English.

CC The invention relates to an expression system which comprises a DNA
 CC molecule encoding Interleukin (IL)-12 and a costimulatory molecule,
 CC operably linked to a promoter that directs the expression of the DNA
 CC molecule. Expression vectors of the invention are useful for in vitro
 CC generation of genetically modified human cancer cells for cancer
 CC therapy. These cells share phenotypes of both antigen presenting cells
 CC and cancer cells and are suitable as a cellular vaccine for certain
 CC types of cancer. Expression vectors are useful for eliciting an anti-
 CC tumour immune response in a individual. They are useful for activating
 CC T cells for immunotherapeutic responses against primary or metastatic
 CC cancers. The present sequence is pIRES-IL12.3-hb7-1 vector DNA.
 CC This vector comprises cytomegalovirus (CMV) promoter and enhancer,
 CC bacteriophage T7 RNA polymerase promoter, human B7-1 DNA, IRES sequence,
 CC human IL-12.3 DNA, bacteriophage T3 RNA polymerase promoter,
 CC Simian virus 40 (SV40) fragment containing polyadenylation signal, fl
 CC origin of replication, Neo^r expression cassette and ampicillin
 CC resistance sequence.
 CC
 XX
 XX Sequence 8644 BP: 2187 A; 2134 C; 2152 G; 2171 T; 0 other:

Query Match 76.1%; Score 1216.6; DB 24; Length 8644;
 Best Local Similarity 85.5%; Pred. No. 0;
 Matches 1392; Conservative 0; Mismatches 204; Indels 33; Gaps 2;

QY 1 ATGCACCTGACGAGTTGTCATCTCTGCTTTCCCTGTTTCTGCGCTCCCTC 60
 DB 1103 ATGTGTCACGACGAGTTGTCATCTCTGCTTTCCCTGTTTCTGCGCTCCCTC 1162
 QY 61 ATGCCCATATGGAGACCTGGAGAAAGATGTTATGTTGTAGAGTGGACCTGGACCCCTGAT 120
 DB 1163 GTGGCCATATGGAGACCTGGAGAAAGATGTTATGTTGTAGAGTGGATTCGATCCGGAT 1222
 QY 121 GCCCCCGGAGAAATGCTGCTCTACCTGCCATACCCCTGAAGAAGATGACATCTTGG 180
 DB 1223 GCCCTCGAGAAATGCTGCTCTACCTGCCATACCCCTGAAGAAGATGATGACCTGG 1282
 QY 181 ACCTGAGTGGAGACGACTGAAGTCTTAGTTCTGCTAAACCTGACCATTCGAAGTAAA 240
 DB 1283 ACCCTGGACGAGACGAGTGGTCTTAGGCTCTGCGCAAAACCCCTGACCATTCGAAGTAAA 1342
 QY 241 GAATTTGGAGATGCTGCCGCTATACCTGCGATTAAGAGGAGCAAGTTTGGAGCGCTGCA 300
 DB 1343 GAGTTTGGAGATGCTGCCGCTATACCTGCGATTAAGAGGAGCGAGTTCTAAGCATTTGC 1402
 QY 301 CTCCTCTTGAATTCACAAAAGAGATGATTTGGTCCATGATATCTTAAGGAACAG 360
 DB 1403 CTCCTCTTGAATTCACAAAAGAGATGATTTGGTCCATGATATCTTAAGGAACAG 1462
 QY 361 AAGGAATTCACAAAAGATGATTTGGTAAATGGAGCAAGATTAATTTGGAGCTTTG 420
 DB 1463 AAGGAATTCACAAAAGATGATTTGGTAAATGGAGCAAGATTAATTTGGAGCTTTG 1522

QY 421 ACATGCTGTGGCTGACGCGCAATCAGTACTGATTTGAATTCAGTGTCAAAAGTAGACAGA 480
 DB 1523 ACCTGTGCTGGTGGCTGACGCGCAATCAGTACTGATTTGAATTCAGTGTCAAAAGTAGACAGA 1582
 QY 481 GGCCTTCTGTACCCCGCAAGGGGTGACATGTGGAGCAGTACTTTCAGCAGAGAGGTC 540
 DB 1583 GGCCTTCTGTACCCCGCAAGGGGTGACGAGTGGAGCTCTACACTCTCTGACAGAGAGTCTC 1642
 QY 541 AGAGTGGACAAAGAGATTTAAGAACTACACAGTGGAGTGTACAGAGGAGGAGTGGCTGC 600
 DB 1643 AGAGGAGCAAAAGAGATTTAAGAACTACACAGTGGAGTGTACAGAGGAGGAGTGGCTGC 1699
 QY 601 CCCCTGCTCCGAGGAGACCTTACCATGAGTGGTGGATGCTGATTTCAAGAGCTCAAG 660
 DB 1700 CCAGCTGCTGAGAGATCTGCTCATTTGAGGTCAATGGTGGATGCTGCTTCAAGAGCTCAAG 1759
 QY 661 TATGAACATACACACAGACCTTCTTCATGAGAGACATCATCAAAACAGACCCACCCACA 720
 DB 1760 TATGAACATACACACAGACCTTCTTCATGAGAGACATCATCAAAACAGACCCACCCACA 1819
 QY 721 AACCTGACGTGAAGCCATTGAAAAATTTCTGCGACGTGAGAGTCAAGTGGAAATACCC 780
 DB 1820 AACCTGACGTGAAGCCATTGAAAAATTTCTGCGACGTGAGAGTCAAGTGGAAATACCC 1879
 QY 781 GACACCTGGAGCAACCCCATCTTCTTCTCCCTGACATTTTGGATACAGAGGCGACAGGC 840
 DB 1880 GACACCTGGAGTATCTCCACATCTCTTCTTCTCCCTGACATTTTGGATACAGAGGCGACAGGC 1939
 QY 841 AAGCAATATGAGAAAAAGAAAGATATGACTCTGCTGGAGCAAGACCTTACGCAAGTCTGTG 900
 DB 1940 AAGCAATATGAGAAAAAGAAAGATATGACTCTTTCACCGACAAAGACCTTACGCAAGTCTGTG 1999
 QY 901 TGGCACAAGATGCAAGATTCGCGGTGCAAGCCGCAAGCCGCTATCTATCTCTGG 960
 DB 2000 TGGCACAAGATGCAAGATTCGCGGTGCAAGCCGCAAGCCGCTATCTATCTCTGG 2059
 QY 961 AGCAGCTGGGCACTGTGTATGATGACAGTGGGCGGTGGCGCGG----- 1004
 DB 2060 AGCAGTGGGCACTGTGTATGATGACAGTGGGCGGTGGCGCGG----- 2119
 QY 1005 -----ATCTAGAATCTTGCAACCCCTACTCATTCGCCGGGTATGTTCCAA 1050
 DB 2120 GCGCGTGAAGCCCATGAGAAACCTCCCGTGGCCACTCCAGACCCAGGAATGTTCCTCA 2179
 QY 1051 TGTTTGAACCACTGCCAACCTTTTGTAGAGCCGTGACGAACACGCTTTCGAAGGCCAGA 1110
 DB 2180 TGCTTTCACCACTGCCAACCTTTTGTAGAGCCGTGACGAACACGCTTTCGAAGGCCAGA 2239
 QY 1111 CAACCTGTAGAAATTTATCTTCTGACCTTGGGAAGATGTGATCAATGACCAAG 1170
 DB 2240 CAACCTGTAGAAATTTATCTTCTGACCTTGGGAAGATGTGATCAATGACCAAG 2299
 QY 1171 GATTAACCCAGACAGTGGAGGCTGCTTACCACTGGAATTAACATGAATGAGATTGC 1230
 DB 2200 GATTAACCCAGACAGTGGAGGCTGCTTACCACTGGAATTAACATGAATGAGATTGC 2359
 QY 1231 CTGCGCTTCCAGAGAGATCTTTGATTAAGAGGAGTGGCTGCTTGGAAAGGCC 1290
 DB 2360 CTAAATTTCCAGAGAGATCTTTGATTAAGAGGAGTGGCTGCTTGGAAAGGCC 2419
 QY 1291 TCTTTTATGAGGCTGCTGCTTGTAGAGCATATGAGAGCACTTGAAGATGTACAGAGATG 1350
 DB 2420 TCTTTTATGAGGCTGCTGCTTGTAGAGCATATGAGAGCACTTGAAGATGTACAGAGATG 2479
 QY 1351 GAATTCAGGCCATGAACCGCAAGCTTTTAATGATTCACCAAGAGGAGATCTTTGATG 1410
 DB 2480 GAGTTTCAAGGCCATGAATGCAAGGCTTCTGATGATCTTAAGAGGAGGAGATCTTTGATG 2539
 QY 1411 CAAAACATGCTGACAGCTATGATGAGCTGTACAGGCGCTGAATTTCAACAGTGTGACT 1470
 DB 2540 CAAAACATGCTGACAGCTATGATGAGCTGTACAGGCGCTGAATTTCAACAGTGTGACT 2599
 QY 1471 GTGCGACAGAAATCTCTCTTGAAGAGCGGATTTTATTAAGACTAAGAGCTCTGCTG 1530

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DB 2600 GTGCCACAAAATCCCTCGTTGAGAACCGGATTTTATATAAACTAAATCAAGCTCTGC 2659
QY 1531 ATACTCTTCATCGCTTTCGAATTCGTGGGAGACATCAATGATGATGTCCTACTTG 1590
DB 2660 ATACTCTTCATCGCTTTCGAATTCGTGGGAGACATGACTATTGATGATGAGCTATCTG 2719
QY 1591 AACCTCTTCC 1599
DB 2720 AATGCTTCC 2728

RESULT 8
AAD31549
ID AAD31549 standard; DNA; 8638 BP.
AC AAD31549;
XX 18-JUN-2002 (first entry)
DT PIRIS-hb7-1-IL12.4 vector DNA.
XX Expression system: Interleukin-12; cancer therapy; cellular vaccine;
KM immunotherapeutic response; IL-12.4; chimeric; human; Simian virus 40;
KM SV40; cytomegalovirus; CMV; ds.
XX Chimeric - Cytomegalovirus.
OS Chimeric - Bacteriophage T7.
OS Chimeric - Homo sapiens.
OS Chimeric - Bacteriophage T3.
OS Chimeric - Rhesus macaque polyoma virus.
XX Chimeric - unidentified.
FH Key
FT enhancer
FT 1.750
FT /tag= a
FT /note= "CMV enhancer; Also serves as a promoter"
FT misc_feature
FT 890..1002
FT /tag= b
FT /note= "Intervening sequence"
FT promoter
FT 1067..1085
FT /tag= c
FT /note= "T7 RNA polymerase promoter"
FT misc_feature
FT 1090..1984
FT /tag= d
FT /note= "Human B7-1 DNA"
FT misc_feature
FT 1090..1954
FT /tag= e
FT /note= "Human B7-1 coding region"
FT RBS
FT 2013..2593
FT /tag= f
FT /note= "IRES sequence"
FT misc_feature
FT 2627..4293
FT /tag= g
FT /note= "Human IL-12.4 DNA"
FT CDS
FT 2640..4283
FT /tag= h
FT /product= "Human IL-12.4 protein"
FT misc_feature
FT 3606..3706
FT /tag= i
FT /note= "Linker of human IL-12.4 sequence"
FT promoter
FT 4392..4413
FT /tag= j
FT /note= "T3 RNA polymerase promoter"
FT polyA_signal
FT 4423..4644
FT /tag= k
FT /note= "SV40 fragment containing polyadenylation signal"
FT rep_origin
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FT /tag= l
FT /note= "f1 origin of replication"
FT misc_feature
FT 5258..6625
FT /tag= m
FT /note= "Neo r expression cassette"
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FT misc_feature 7036..7896
FT /tag= n
FT /note= "Ampicillin resistance"
FT US2002018767-A1.
PN 14-FEB-2002.
PD 10-APR-2001; 2001US-0828825.
PE 27-JUL-2000; 2000KR-0043498.
XX (LEES/) LEE S.
XX (KIMH/) KIM H.
XX Lee S, Kim H;
PT WPI: 2002-239247/29.
DR P-PSDB; AAE19821.
XX New expression system, useful as vaccine for treating cancer, comprises
PT DNA molecule encoding Interleukin-12 and costimulatory molecule,
PT operably linked to promoter that directs the expression of DNA molecule
PS Example 1; Page 38-43; 76pp; English.
XX The invention relates to an expression system which comprises a DNA
CC molecule encoding Interleukin (IL)-12 and a costimulatory molecule,
CC operably linked to a promoter that directs the expression of the DNA
CC molecule. Expression vectors of the invention are useful for in vitro
CC generation of genetically modified human cancer cells for cancer
CC therapy. These cells share phenotypes of both antigen presenting cells
CC and cancer cells and are suitable as a cellular vaccine for certain
CC types of cancer. Expression vectors are useful for eliciting an anti
CC tumour immune response in a individual. They are useful for activating
CC T cells for immunotherapeutic responses against primary or metastatic
CC cancers. The present sequence is PIRIS-hb7-1-IL12.4 vector DNA.
CC This vector comprises cytomegalovirus (CMV) promoter and enhancer,
CC bacteriophage T7 RNA polymerase promoter, human B7-1 DNA, IRES sequence,
CC human IL-12.4 DNA, bacteriophage T3 RNA polymerase promoter,
CC Simian virus 40 (SV40) fragment containing polyadenylation signal, f1
CC origin of replication, Neo r expression cassette and ampicillin
CC resistance sequence.
XX Sequence 8638 BP; 2184 A; 2130 C; 2156 G; 2168 T; 0 other;
SQ
Query Match 75.1%; Score 1201.6; DB 24; Length 8638;
Best Local Similarity 84.7%; Pred. No. 0;
Matches 1392; Conservative 0; Mismatches 204; Indels 48; Gaps 2;
QY 1 ATGCACCCCTCAGCAGTGTGTCATCTGCTGCTTCCCTGTTTGCTGCGCTCCCTC 60
DB 2640 ATGTGTCACCCAGCAGTGTGTCATCTGCTGCTTCCCTGTTTGCTGCGATCTCCCTC 2699
QY 61 ATGGCCATATGGGAAGCTGGAAGAAGATGTTATGTTAGAGCTTGAGCTGCACCCGTAT 120
DB 2700 GTGGCCATATGGGAAGCTGGAAGAAGATGTTATGTTAGAGCTTGAGCTGCATCCGAT 2759
QY 121 GCCCGCGAGAAATGTGTGCTCTCACCTGCCATACCCTCGAAGGAAGATGATCACTGTGG 180
DB 2760 GCCCGCGAGAAATGTGTGCTCTCACCTGCCATACCCTCGAAGGAAGATGATCACTGTGG 2819
QY 181 ACCCTGAGCGAGAGCAAGTAAAGTCTGAGTGTGTAAGAACTGACCTGCAAGTCAGAA 240
DB 2820 ACCCTGAGCGAGAGCAAGTAAAGTCTGAGTGTGTAAGAACTGACCTGCAAGTCAGAA 2879
QY 241 GAATTTGAGATGCTGGCCAGTATACCTGCCATAAAGAGGCAAGTCTTGAAGCCGCTCA 300
DB 2880 GAGTTTGAGATGCTGGCCAGTATACCTGCCATAAAGAGGCAAGTCTTGAAGCCGCTCA 2939
QY 301 CTCCTGTTGATTCACAAAAGAGAGATGGAATTTGTGCTCAGTATATCTTAAAGAACAG 360
||||| ||| ||||||||| ||||||||| ||||||||| ||||||||| ||||||||| |||
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Db 2940 CTCCTGCGTCGTCACAAAAGAGATGGAATTGGTGCAGTATATTTAAAGACGAG 2999
 QY 361 AAGAAATTCAAAATTAAGATCTTTCGAATGATGAGCGCAAGAAATATTTGTGAGCTTTC 420
 Db 3000 AAAGAAATCAAAAATTAAGACCTTTCTAAGATGCGAGCGCAAGAAATATTTCTGAGCGTTTC 3059
 QY 421 ACATGCTGTGAGTGCAGGCAATCAGTACTGATTTGAAATTCAGTGCAGAACTAGACAGA 480
 Db 3060 ACGTGTGTGCTGAGGAGCAATCAGTACTGATTTGACATTTGAGTGTGCAGAAAGCTGACAGA 3119
 QY 481 GGCCTTCTGAGCCCGCAAGCGGTGACATGTTGAGCAGTACACACTTTCAGCAGAGAGGTC 540
 Db 3120 GGCCTTCTGAGCCCGCAAGCGGTGAGCTGTGAGCTGTGACACTCTCTCTGAGAGAGAGTTC 3179
 QY 541 AAGATGACACATGAGGATATATAGAAATACAGCTGAGTGTGACAGAGAGGCTACTGCTGC 600
 Db 3180 AAGAGGGGACACAGAGAGATAT--GAGTACTAGTGTGAGTGTGCGAGAGGACATGCTGCTGC 3236
 QY 601 CCGCTGTGCGAGAGAGACCTACCCATCGAGTGTGCTGATGCTATTTACAGAGCTCAAG 660
 b 3237 CCAGCGTGTGAGGAGAGTCTGTCCATTGAGTGTGATGTGATGCGCTTCAGAAAGCTCAAG 3296
 QY 661 TATGAAACTACACGACGAGCTTCTTCATCAGAGACATCATCAACGAGACCCACACA 720
 Db 3297 TATGAAACTACACGACGAGCTTCTTCATCAGAGACATCATCAACCTGACCCACACA 3356
 QY 721 AACCTGCAGCTGAGGCAATTTGAAATTCCTGCGACAGTGTGAGTGTGAGTGTGAGATACCC 780
 Db 3357 AACCTGCAGCTGAGGCAATTTGAAATTCCTGCGACAGTGTGAGTGTGAGTGTGAGATACCC 3416
 QY 781 GACACTGTGAGGACCCGACATTTCTCTGCTGACATTTTGCATATACAGGCGGAGG 840
 Db 3417 GACACTGTGAGTACTGTACATTTCTCTGCTGACATTTTGCATATACAGGCGGAGG 3476
 QY 841 AAGACATATGAGAAAGAAAGATAGACTGTGCTGCGACAGAACCTTCACCAAGGTGCTG 900
 Db 3477 AAGACATATGAGAAAGAAAGATAGACTGTGCTGCGACAGAACCTTCACCAAGGTGCTG 3536
 QY 901 TGGCACAGGATGTCCAGATTCGCGGTGCAAGCGGAGAGCTGACTATAGTTCATCTCTG 960
 Db 3537 TGGCGTCAAAATGTCCAGATTTAGCGGTGCGCGCTCAGAGACCTGACTATAGTTCATCTCTG 3596
 QY 961 AAGCATGTGCGATCTGTGTGATGCACTGTGTGGGTGTGGCGCGG----- 1004
 Db 3597 AAGCATGTGCGATCTGTGTGATGCACTGTGTGGGTGTGGCGCGG----- 3656
 QY 1005 -----ATCTAGAAACCTTGGCAACCCCTACTGCTCATCC 1035
 Db 3657 GAGCGTGCAGAGCGGTGGCGGTGGAAAGCCCATGGAGAAACCTCGCGGTGGCACTGCAGAC 3716
 QY 1036 GAGCGTATGTTCCAAATGTTTGAAAGCCGTCGCAAGCTTGTGAGAGCGCTTCAGCAAGCAG 1095
 Db 3717 CCAGGAATGTTCCAAATGTTTGAAAGCCGTCGCAAGCTTGTGAGAGCGCTTCAGCAAGCAG 3776
 QY 1096 CTTTCAGAGCGCCGACAACTCTAGATATATTCCTGACTTCCGAGACATTTGATCAT 1155
 Db 3777 CTTTCAGAGCGCCGACAACTCTAGATATTTTACCCCTTGACATTTCTGAAGAGATTTGATCAT 3836
 QY 1156 GAGAGATATCAGAAAGATTAAGACGACAGTGTGAGAGCGCTTACCACTGGAATTAACC 1215
 Db 3837 GAGAGATATCAGAAAGATTAAGACGACAGTGTGAGAGCGCTTACCACTGGAATTAACC 3896
 QY 1216 ATGAAATGAGTGTGCTGTGCTTCCAGAGAGATCTTTGATATACATACAGGAGTGTGCTG 1275
 Db 3897 AAGAAATGAGTGTGCTGTGCTTCCAGAGAGATCTTTGATATACATTAAGGAGTGTGCTG 3956
 QY 1276 GGCCTTGTGAAGGCTCTTTTATGAGCGTGTGCTTACGAGCTATCATAGAGAGCTTG 1335
 Db 3957 GGCCTTGTGAAGGAGCTCTTTTATGAGCGCTGTGCTTACGAGCTATCATAGAGAGCTTG 4016
 QY 1336 AAGATGTATCAGATGTGAATTTCAAGGCGCATGAACGCAAAAGCTTTTATGAGTGTGAGGAG 1395
 Db 4017 AAGATGTATCAGATGTGAGTGTGAAGGCGCATGAATGCAAAAGCTTCTGATGCATCTTAAGAGG 4076

QY 1396 CAGATCTTTCTGATGATCAAAACATGCTGACAGCATATGATGAGCTGTACAGGCGCTGAAT 1455
 Db 4077 CAGATCTTTCTGATGATCAAAACATGCTGACAGCATATGATGAGCTGTACAGGCGCTGAAT 4136
 QY 1456 TTCAACAGCTGTGAGTGTGCGACAGAAATGCTCTGGAAGAGCGGATTTTATAAAGCT 1515
 Db 4137 TTCAACAGCTGTGAGTGTGCGACAAATATGCTCTGGAAGAGCGGATTTTATAAAGCT 4196
 QY 1516 AAAATCAAGCTGTGATCTTCTTCATGCTTTTCAGAAATTCGTGCGGTGACCATCAATAGA 1575
 Db 4197 AAAATCAAGCTGTGATCTTCTTCATGCTTTTCAGAAATTCGTGCGGTGACCATCAATAGA 4256
 QY 1576 ATGATGTCTACTTGAACCTCTTCC 1599
 Db 4257 GTGATGAGCTATCTGAATGCTTCC 4280
 RESULT 9
 AAD31550
 ID AAD31550 standard; DNA; 8659 bp.
 XX
 AC AAD31550:
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE pIRES-IL12.4-hb7-1 vector DNA.
 XX
 KW Expression system; Interleukin-12; cancer therapy; cellular vaccine;
 KW Immunotherapeutic response; IL-12.4; chimeric; human; Simian virus 40;
 KW SV40; cytomegalovirus; CMV; ds.
 XX
 OS Chimeric - Cytomegalovirus.
 OS Chimeric - Bacteriophage T7.
 OS Chimeric - Homo Sapiens.
 OS Chimeric - Bacteriophage T3.
 OS Chimeric - Rhesus macaque polyoma virus.
 OS Chimeric - unidentified.
 XX
 FH Key
 FH enhancer
 FT Location/Qualifiers
 FT 1..750
 FT /tag= a
 FT /note= "CMV enhancer; Also serves as a promoter"
 FT 1067..1085
 FT /tag= b
 FT /note= "T7 RNA polymerase promoter"
 FT 1090..2756
 FT /tag= c
 FT /note= "Human IL-12.4 DNA"
 FT 1103..2746
 FT /tag= d
 FT /product= "Human IL-12.4 protein"
 FT 2087..2146
 FT /tag= e
 FT /note= "Linker of human IL-12.4 sequence"
 FT 2782..3362
 FT /tag= f
 FT /note= "IRES sequence"
 FT 3399..4293
 FT /tag= g
 FT /note= "Human B7-1 DNA"
 FT 4413..4434
 FT /tag= h
 FT /note= "T3 RNA polymerase promoter"
 FT 4444..4665
 FT /tag= i
 FT /note= "SV40 fragment containing polyadenylation signal"
 FT 4760..5215
 FT /tag= j
 FT /note= "f1 origin of replication"
 FT 5279..6646
 FT /tag= k
 FT /note= "Neo r expression cassette"

AC AAX35625:
XX 09-JUL-1999 (first entry)
XX Nucleic acid encoding canine Interleukin-12 (IL-12).
DE Interleukin-12; IL-12; dog; cat; immune disease; CaIl12; heterodimer;
KW tumour; skin disease; infectious disease; allergic disease; ds.
XX
OS Canis sp.
XX
FH Key Location/Qualifiers
FT 1..990
FT CDS /*tag= a
XX
XX JP11106350-A.
XX
PD 20-APR-1999.
XX
XX 15-MAY-1998; 98JP-0133345.
XX
PR 07-AUG-1997; 97JP-0213755.
XX 16-MAY-1997; 97JP-0127690.
XX
XX (TORA) TORAY IND INC.
XX
XX WPI: 1999-308068/26.
XX P-PSDB: AAY02342.
XX
XX
XX A prevention and treating agent containing interleukin 12 (CaIl12) -
PT for prevention and treatment of dog and cat immune diseases
XX
XX Claim 1: Page 14-15; 16pp; Japanese.
XX
XX The present sequence encodes canine interleukin-12 (IL-12). The
CC specification describes a method for the prevention and treatment
CC of dog and cat immune diseases. The treatment used an agent comprising
CC dog IL-12 (CaIl12) proteins to form a heterodimer. The agent is
CC useful for preventing and treating dog and cat immune diseases,
CC including tumours, skin diseases, infectious diseases and allergic
CC diseases.
XX
XX Sequence 990 BP: 279 A: 244 C: 249 G: 218 T: 0 other:
SO
Query Match 61.5%: Score 983.8; DB 20; length 990;
Best Local Similarity 99.8%: Pred. No. 5.1e-291;
Matches 985; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 361 AAGAAATCCAAAATAAGATCTTCTGAAATGTGAGGCAAGAATATTATTCGAGCTTTC 420
OY 421 ACATGCTGTGGCTGACGGCAATGACTGATTTTGAATTCAGTGTCAAAAAGTAGCA 480
DB 421 ACATGCTGTGGCTGACGGCAATGACTGATTTTGAATTCAGTGTCAAAAAGTAGCA 480
OY 481 GCGTCTCTGACCCCAAGGGGTGACATGTGGAGCAGTGCACCTTTCAGCAGAGGGTTC 540
DB 481 GCGTCTCTGACCCCAAGGGGTGACATGTGGAGCAGTGCACCTTTCAGCAGAGGGTTC 540
OY 541 AGAGTGAACAACAGGATTAATAGAGTACACAGTGAAGTGTGACAGAGGGAGGAGTTC 600
DB 541 AGAGTGAACAACAGGATTAATAGAGTACACAGTGAAGTGTGACAGAGGGAGGAGTTC 600
OY 601 CCTCTGCGGAGAGAGGCTTACCCATCGAGGTCGTGTGATGCTATTTCACAGCTCAAG 660
DB 601 CCTCTGCGGAGAGAGGCTTACCCATCGAGGTCGTGTGATGCTATTTCACAGCTCAAG 660
OY 661 TATGAAGACTACACGAGCTTCTTCATGAGAGCATCATCAACGAGCCAGCCAGCA 720
DB 661 TATGAAGACTACACGAGCTTCTTCATGAGAGCATCATCAACGAGCCAGCCAGCA 720
OY 721 AACCTGACGCTGAAGCCATTGAAAAATTCTCGGACGTCGAGGTCAGCTGGGAATACCC 780
DB 721 AACCTGACGCTGAAGCCATTGAAAAATTCTCGGACGTCGAGGTCAGCTGGGAATACCC 780
OY 781 GACACCTGAGACACCCCATCTTCTACTTCTCCCTGACATTTTGCATACAGCCAGGGC 840
DB 781 GACACCTGAGACACCCCATCTTCTACTTCTCCCTGACATTTTGCATACAGCCAGGGC 840
OY 841 AAGAAACAAATAGAAAAAAGATAGACTGCGTGACAGACCTCGCAAGGTCGTG 900
DB 841 AAGAAACAAATAGAAAAAAGATAGACTGCGTGACAGACCTCGCAAGGTCGTG 900
OY 901 TGCCACAAGATGCCACAGATCCGCTGCAAGCCGAGACCCCTACTATATTTCATCTGG 960
DB 901 TGCCACAAGATGCCACAGATCCGCTGCAAGCCGAGACCCCTACTATATTTCATCTGG 960
OY 961 AGCGACTGGCATCTGTGTCTCATGAGT 987
DB 961 AGCGACTGGCATCTGTGTCTCTGCACT 987
RESULT 12
AAX03162
ID AAX03162 standard; cDNA to mRNA; 990 BP.
XX
AC AAX03162:
XX
DT 30-MAR-1999 (first entry)
XX
DE Nucleic acid encoding canine interleukin 12.
XX
XX Canine; interleukin 12; IL-12; feline; immunological disease; tumour;
KW skin disease; viral infection; allergic disease; breast tumour;
KW osteinophilic granuloma; epidermoid tumour; skin tumour; lipoma;
KW otitis externa; dermatitis; eczema; fungal skin disease; pyoderma;
KW allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
KW dog Parvovirus infection; distemper virus; cat plaque virus infection;
KW feline leukaemia; allergy; pollinosis; ds.
XX
OS Canis sp.
XX
FH Key Location/Qualifiers
FT 1..990
FT CDS /*tag= a
FT /product= interleukin_12
XX
XX WC9851327-A1.
XX
PD 19-NOV-1998.

XX 07-MAY-1998: 98W0-JP02031.
 PF
 XX
 PR 15-MAY-1997: 97JP-0127690.
 XX
 PA (TORA) TOKAY IND INC.
 XX
 PI Okano F., Satoh M., Yamada K;
 XX
 DR WPI: 1995-070100/06.
 DR P-PSDB: AAM84373.
 XX
 PF New therapeutic and prophylactic agents - comprise
 PF genetically-engineered canine interleukin 12, used to treat, e.g.
 PF canine and feline immunological diseases
 XX
 PS Claim 1: Page 30-32; 45pp; Japanese.
 XX
 CC The present sequence encodes a canine interleukin 12 (IL-12) protein.
 CC The IL-12 protein can be used in therapeutic or prophylactic agents.
 CC The agents can be used to prevent and treat canine and feline
 CC immunological diseases including dog and cat tumours, skin diseases,
 CC viral infections and allergic diseases, especially tumours, breast
 CC tumour, oesthiophilic granuloma, epidermoid tumour, skin tumour, lipoma,
 CC othematoma, pneumoedema, skin soft pedicled soft tumour and anal
 CC tumour; skin diseases, otitis externa, dermatitis, eczema, fungal
 CC diseases of the skin, pyoderma, allergic dermatitis, nettle rash,
 CC traumatic dermatitis and hair loss; infections; dog parvovirus infection
 CC and distemper virus; cat plague virus infection and feline leukaemia, and
 CC allergic diseases, e.g. pollinosis.
 CC
 XX Sequence 990 BP: 279 A; 244 C; 249 G; 218 T; 0 other;

Query Match 61.5%; Score 983.8; DB 20; length 990;
 Best Local Similarity 99.8%; Pred. No. 5,1e-291;
 Matches 985; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGACCCCTGAGCAGTGTGTCATCTGCTGTTTCCCTGCTGTTGCGCCCTG 60
 DB 1 ATGCACTCTGACACATTTGTGTCATCTGCTGTTTCCCTGCTGCTCCCTG 60
 QY 61 ATGCCCATATGGAGACTGAGAAAGATCTTATGTTGTAGAGTGGACTGGCCCTGAT 120
 DB 61 ATGCCATATGGAGACTGAGAAAGATCTTATGTTGTAGAGTGGACTGGCCCTGAT 120
 QY 121 GCGCCCGGAGAAATGCTGCTCTCAGCTGCCATACCCCTGAAGAAGATGACTGCTGG 180
 DB 121 GCGCCCGGAGAAATGCTGCTCTCAGCTGCCATACCCCTGAAGAAGATGACTGCTGG 180
 Y 181 ACCTGACGCGAGAGCAGTGAAGTCTAGATTCTGTGTAAGCTGTGAGCATCCAGTCAAA 240
 DB 181 ACCTGACGCGAGAGCAGTGAAGTCTAGATTCTGTGTAAGCTGTGAGCATCCAGTCAAA 240
 QY 241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATTAAGAGAGCAAGCTTCTGAGCCGCTCA 300
 DB 241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATTAAGAGAGCAAGCTTCTGAGCCGCTCA 300
 QY 301 CTCCTGTGATTCACAAAAGAGATGGAATTTGCTGCACCTGATATCTTAAAGCAAGAG 360
 DB 301 CTCCTGTGATTCACAAAAGAGATGGAATTTGCTGCACCTGATATCTTAAAGCAAGAG 360
 QY 361 AAAAGATTC:AAAAGATTAAGATCTTTCTGAATGTGAGGCAAGGAATTAATCTGAGAGCTTTC 420
 DB 361 AAAAGATTC:AAAAGATTAAGATCTTTCTGAATGTGAGGCAAGGAATTAATCTGAGAGCTTTC 420
 QY 421 ACATGCTGCTGCTGAGCGGCAATCAGTACTGATTTGAATTCAGTCTTCTGAGAGCTTTC 480
 DB 421 ACATGCTGCTGCTGAGCGGCAATCAGTACTGATTTGAATTCAGTCTTCTGAGAGCTTTC 480
 QY 481 GGCTTCTGAGCGCTCAAGGGGTGACATGTGAGAGCAGTTCACACTTTCAGCAGAGAGGGTGC 540
 DB 481 GGCTTCTGAGCGCTCAAGGGGTGACATGTGAGAGCAGTTCACACTTTCAGCAGAGAGGGTGC 540

QY 541 AGAGTGGACACAGGAGATTATAGAAGTACACAGTGGATGTCAGAGGCGAGTGCCTGC 600
 DB 541 AGAGTGGACACAGGAGATTATAGAAGTACACAGTGGATGTCAGAGGCGAGTGCCTGC 600
 QY 601 CCTCTGCGCGAGAGAGCGCTTACCCATTCGAGCTGTGCTGGATGCTATTTCACAAGCTCAAG 660
 DB 601 CCTCTGCGCGAGAGAGCGCTTACCCATTCGAGCTGTGCTGGATGCTATTTCACAAGCTCAAG 660
 QY 661 TATGAAAACTACACAGCAGCAGCTTCTTCATGACAGACATTCATTAACACAGACCACACACA 720
 DB 661 TATGAAAACTACACAGCAGCAGCTTCTTCATGACAGACATTCATTAACACAGACCACACACA 720
 QY 721 AACCTGACACCTGACAGCCATTTGAAAAATTCGTGGCAGCTGGAGTGCAGCTGGGAATTAACCC 780
 DB 721 AACCTGACACCTGACAGCCATTTGAAAAATTCGTGGCAGCTGGAGTGCAGCTGGGAATTAACCC 780
 QY 781 GACACCTGAGAGCAGCCCATTTCTACCTTCTGCTGACATTTTGCATACAGGCCAGGCG 840
 DB 781 GACACCTGAGAGCAGCCCATTTCTACCTTCTGCTGACATTTTGCATACAGGCCAGGCG 840
 QY 841 AAGACCAATAGAGAAAGAAAGATAGACTCTGCTGGACAAGACCTCAGCCAGAGTCTG 900
 DB 841 AAGAACCAATAGAGAAAGAAAGATAGACTCTGCTGGACAAGACCTCAGCCAGAGTCTG 900
 QY 901 TGGCCAAAGCATGCCAAGATCCGCGGCAAGCCCGAGACCGGTACTATGATTCATCTGG 960
 DB 901 TGGCCAAAGCATGCCAAGATCCGCGGCAAGCCCGAGACCGGTACTATGATTCATCTGG 960
 QY 961 ACCGACTGGGCATCTGTCTCATGCACT 987
 DB 961 ACCGACTGGGCATCTGTCTCTGCACT 987

RESULT 13
 AA164388
 ID AA164388 standard; DNA; 990 BP.
 XX
 AC AA164388;
 XX
 DT 23-NOV-2001 (first entry)
 DE
 XX Canine coding sequence #3.
 KW Canine; dog; immunostimulant; interleukin 12; IL12; immunopathy; ds.
 XX
 OS Canis familiaris.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..990
 FT sig_peptide /*tag= a
 FT mat_peptide /product= "Canine protein #1"
 FT /tag= b
 FT /tag= 67..987
 FT /*tag= c
 PN JP2001161378-A.
 PD 19-JUN-2001.
 XX
 PF 26-SEP-2000; 2000JP-0292946.
 PR 01-OCT-1999; 99JP-0281234.
 XX
 PA (TORA) TOKAY IND INC.
 XX
 DR WPI: 2001-592466/67.
 DR P-PSDB: AAG65482.
 XX
 PF Preparation of a highly pure protein, interleukin 12, a protein
 PF inhibiting the activity of interleukin 12, and a treating agent and a
 PF treating method for immunopathy of mammalian

PS Claim 6; Page 16-17; 21pp; Japanese.

CC The present invention relates to a method for the preparation of a highly
CC pure protein in which interleukin 12 (IL12) and/or a protein inhibiting
CC the activity of IL12 is contacted to an ion exchanging carrier and/or a
CC pigment carrier to get IL12 and/or a protein inhibiting the activity of
CC IL12. The protein is used as a preventive agent for dog immunopathy. The
CC present sequence was used in the method of the present invention.

Sequence 990 BP; 279 A; 244 C; 249 G; 218 T; 0 other;

Query Match	61.5%	Score 983.8	DB 22	Length 990
Best Local Similarity	99.8%	Pred. No. 5.1e-291		
Matches 985	Conservative	0	Mismatches 2	Indels 0
				Gaps 0

OY	1	ATTAACCTGACGATGGTGTGATCTCTGATTTTCCCTGATTTTGGTGGGCTCTCCCTTC	60
	1	ATGATCTCTGACGATGGTGTGATCTCTGATTTTCCCTGATTTTGGTGGGCTCTCCCTTC	60
	61	ATGGCCATTATGGGAACGTGGAAGAAAGATGTTTATGTTGTAGAGTTGGACGTGGACCCGTGAT	120
	61	ATGGCCATTATGGGAACGTGGAAGAAAGATGTTTATGTTGTAGAGTTGGACGTGGACCCGTGAT	120
OY	121	GCCTCCGAGCAAAATGTTGGTCTTCACCTGGCATACCCCTGAAGAAGATGCATCTACTGG	180
	121	GCCTCCGAGCAAAATGTTGGTCTTCACCTGGCATACCCCTGAAGAAGATGCATCTACTGG	180
OY	181	ACCTCAGCGCAGACCACTGAAGTCTGATGGTTCGTGTAAACCTGTGACATCTCCAAAGTCCAA	240
	181	ACCTCAGCGCAGACCACTGAAGTCTGATGGTTCGTGTAAACCTGTGACATCTCCAAAGTCCAA	240
OY	241	GAATTTGAGATGCTGGCCAGTATACCTGCCATTAAGGAGCAAGCTTGTGAGACCCCTCA	300
	241	GAATTTGAGATGCTGGCCAGTATACCTGCCATTAAGGAGCAAGCTTGTGAGACCCCTCA	300
OY	301	CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCATGATATCTTTAAAGAAACAG	360
	301	CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCATGATATCTTTAAAGAAACAG	360
OY	361	AAACAATCCAAAAATTAAGATCTTCTCAATATGGAGCAAGAAATATCTGGACGTTTC	420
	361	AAACAATCCAAAAATTAAGATCTTCTCAATATGGAGCAAGAAATATCTGGACGTTTC	420
OY	421	ACATGCTGTGGGCTGAGCGCAATCAGTACGATTTGAAATTCAGTGTCAAAAATAGACAGA	480
	421	ACATGCTGTGGGCTGAGCGCAATCAGTACGATTTGAAATTCAGTGTCAAAAATAGACAGA	480
OY	481	GGCTTCTCTGACCCCAAGGGGTGACATGTGGACAGTGCACCTTTCAGCAGAGAGGGTTC	540
	481	GGCTTCTCTGACCCCAAGGGGTGACATGTGGACAGTGCACCTTTCAGCAGAGAGGGTTC	540
OY	541	AGATGTGACAACACAGGATTTTAAGAAATACACAGTGAAGTGCAGAGGGCACTGGCTGC	600
	541	AGATGTGACAACACAGGATTTTAAGAAATACACAGTGAAGTGCAGAGGGCACTGGCTGC	600
OY	601	CCCTCTGCGGAGAGAGCCTTACCCTATGAGGTGCTGTGTGATCTCTATTCAAGATCTAAG	660
	601	CCCTCTGCGGAGAGAGCCTTACCCTATGAGGTGCTGTGTGATCTCTATTCAAGATCTAAG	660
OY	661	TATGAAACATACACACAGACCTTTCATGAGACATCATCAAAACAGACCCACCCACA	720
	661	TATGAAACATACACACAGACCTTTCATGAGACATCATCAAAACAGACCCACCCACA	720
OY	721	AACCTGAGCTGAAAGCCATTGAAAAATTTTCGGACAGTGAAGTTCAGTGGGGAATACCC	780
	721	AACCTGAGCTGAAAGCCATTGAAAAATTTTCGGACAGTGAAGTTCAGTGGGGAATACCC	780
OY	781	GACACCTGGAGACACCCCACTTCTACTCTTCCCTGACATTTTGGCATACAGGCCACAGGGC	840
	781	GACACCTGGAGACACCCCACTTCTACTCTTCCCTGACATTTTGGCATACAGGCCACAGGGC	840
OY	841	AAGACAAATGAGAAAAAAGATAGACTTGGCTGTGACAGACCTTAGCCAAAGTCTGTG	900
	841	AAGACAAATGAGAAAAAAGATAGACTTGGCTGTGACAGACCTTAGCCAAAGTCTGTG	900

Accession	Sequence	Position
Db	841 AAGAACTATAGACAAAAGAAAGATATAGACTCTCGCTGGCAAGACCTGACGCAAGTGCTG	900
Oy	901 TGCCACGAAGATGCCCAAGATCCGGGTGCAAAGCCGACAGCTACTATATTCATCTCG	960
Db	901 TGCCACGAAGATGCCCAAGATCCGGGTGCAAAGCCGACAGCTACTATATTCATCTCG	960
Oy	961 AGCGACTGGGCATCTGTGTCTATGTCAGT	987
Db	961 AGCGACTGGGCATCTGTGTCTATGTCAGT	987

RESULT 14
AAV13816
ID AAV13816 standard; cDNA to mRNA; 990 BP.

AC	AAV13816:	
XX		
DT	14-MAY-1998 (first entry)	
XX		
DE	Canine IL-12 P40 subunit cDNA.	
XX		
KW	Canine; interleukin-12 P40 subunit; IL-12 P40 subunit; antitumour	
KM	antiviral; vaccine adjuvant; ds.	
XX		
OS	Canis sp.	
XX		
FH		location/Qualifiers
FT	key	1..990
FT	CDS	/*tag= a
FT		/product= interleukin-12_P40_subunit

CC The present sequence encodes canine interleukin-12 (IL-12) p40
CC subunit. A canine IL-12 comprising a p40 and p35 subunit is capable
CC of inducing an antiviral activating factor and the expression of
CC class II MHC molecules in canine tumour cells, stimulating
CC proliferation of canine blastogenic lymphocytes and activating
CC canine leukocytes to inhibit canine tumour cells. The canine IL-12
CC can be used in veterinary medicines, e.g. antitumour, antiviral and
CC vaccine adjuvant activities are expected.

Sequence 990 BP; 278 A; 243 C; 251 G; 218 T; 0 other;

Query Match	60.8%	DB 19	Length	990
Best Local Similarity	99.1%	Pred. No. 1.4e-287		
Matches 978: Conservative	0	Mismatches 9	Indels	0
			Gaps	0

QY	1	ATGACGCTGAGCAGTGGTGCATATCTCCGTGTTTCCCTGCTTGGCGGCTCCGCC	60
		1	ATGCTGACCAAGCAGTGGTGCATCTCTGGGTTTCCCTCGCTTGGCGGCTCTCCGCC
Db	1	ATGCTGACCAAGCAGTGGTGCATCTCTGGGTTTCCCTCGCTTGGCGGCTCTCCGCC	60
QY	61	ATGACCATATGCGAAGCTGGAGAAAGATCTTTATGTTCTAGAGTTGGAGCTGGACCCGTAT	120
		61	ATGGCCCATATGCGAAGCTGGAGAAAGATCTTTATGTTCTAGAGTTGGAGCTGGACCCGTAT
Db	61	ATGGCCCATATGCGAAGCTGGAGAAAGATCTTTATGTTCTAGAGTTGGAGCTGGACCCGTAT	120

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QY 121 GCCCCGAGAAATGATGCTGCTCCACCTGCCATATCCCTGGAAGAAATGACATCACTTGG 180
XX |||||||
OS 121 GGGCCCGAAGAAATGATGCTGCTCCACCTGCCATATCCCTGGAAGAAATGACATCACTTGG 180
XX |||||||
QY 181 ACCCTGAGTCAGAGCAGTGAAGTCTAGGTTCTGG1AAAACCTCTGACCATCCAGTCCAAA 240
XX |||||||
Db 181 ACCCTGAGTCAGAGCAGTGAAGTCTAGGTTCTGG1AAAACCTCTGACCATCCAGTCCAAA 240
XX |||||||
QY 241 GAATTTGAGATGCTGGCCAGTATACCTGCTCCATAAAGAGGCAAGGTTCTGAGCCGCTCA 300
XX |||||||
Db 241 GAATTTGAGATGCTGGCCAGTATACCTGCTCCATAAAGAGGCAAGGTTCTGAGCCGCTCA 300
XX |||||||
QY 301 CTCCTGTTGATTCACAAAAACAGATGGAATTTGCTGCACGTGATCTTAAAGAACAG 360
XX |||||||
Db 301 CTCCTGTTGATTCACAAAAACAGATGGAATTTGCTGCACGTGATCTTAAAGAACAG 360
XX |||||||
QY 361 AAAGATCCAAAAATAGATCTTTCTGAAATGTGAGGCAAGAAATTAATTTCTGACGTTTC 420
XX |||||||
Db 361 AAAGATCCAAAAATAGATCTTTCTGAAATGTGAGGCAAGAAATTAATTTCTGACGTTTC 420
XX |||||||
QY 421 ACATGCTGCTGGCTGACCGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTACAGA 480
XX |||||||
Db 421 ACATGCTGCTGGCTGACCGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTACAGA 480
XX |||||||
QY 481 GGCTTCTGACCCCGCAAGGGGTGACATGTGTGAGCAGTGACACTTTGACGAGAGGGTTC 540
XX |||||||
Db 481 GGCTTCTGACCCCGCAAGGGGTGACATGTGTGAGCAGTGACACTTTGACGAGAGGGTTC 540
XX |||||||
QY 541 AGAGTGGACAAACAGGGATTTATAGAAGTACACAGTGGAGTGTGACGAGCGCAGTGCCTGC 600
XX |||||||
Db 541 AGAGTGGACAAACAGGGATTTATAGAAGTACACAGTGGAGTGTGACGAGCGCAGTGCCTGC 600
XX |||||||
QY 601 CCCTCTGCGGAGAGAGGCTACCCATCGAGTCTGTGTGATGCTATTTCACAAGCTCAAG 660
XX |||||||
Db 601 CCCTCTGCGGAGAGAGGCTACCCATCGAGTCTGTGTGATGCTATTTCACAAGCTCAAG 660
XX |||||||
QY 661 TATGAAACTACATCAGCAGCTTCTTCATCAGAGCATCATCAAAACCAACCCATCCGACA 720
XX |||||||
Db 661 TATGAAACTACATCAGCAGCTTCTTCATCAGAGCATCATCAAAACCAACCCATCCGACA 720
XX |||||||
QY 721 AACCTGACGCTGAAGCCATTTGAAAAATCTCGGACGCTGAGCTGAGTGGGAATACCCC 780
XX |||||||
Db 721 AACCTGACGCTGAAGCCATTTGAAAAATCTCGGACGCTGAGCTGAGTGGGAATACCCC 780
XX |||||||
QY 781 GACACCTGAGAGCCTCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCACGCGC 840
XX |||||||
Db 781 GACACCTGAGAGCCTCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCACGCGC 840
XX |||||||
QY 841 AAGACATATAGAGAAAGAAAGATAGACTCTGCTGGATACAGCTCAAGCCAAAGGCTGG 900
XX |||||||
Db 841 AAGACATATAGAGAAAGAAAGATAGACTCTGCTGGATAGAAACCTCAAGCCAAAGGCTGG 900
XX |||||||
QY 901 TGCCACAAGGATGCCAAGATCGGCTGCCAAGGCCGAGATCCCTACTATATAGTTCAATCTGG 960
XX |||||||
Db 901 TGCCACAAGGATGCCAAGATCGGCTGCCAAGGCCGAGATCCCTACTATATAGTTCAATCTGG 960
XX |||||||
QY 961 AGCGACTGGCATCTGTGTGATGCACT 987
XX |||||||
Db 961 AGCGACTGGCATCTGTGTGCTGCACT 987
XX |||||||

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RESULT 15
AAX35615
ID AAX35615 standard: cDNA to mRNA; 990 BP.
XX
AC AAX35615;
XX
DT 09-JUN-1999 (first entry)
XX
DE Nucleic acid encoding canine Interleukin-12 (IL-12).
XX
KW Interleukin-12; IL-12; dog; cat; immune disease; CxIL12; heterodimer;

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KW tumour; skin disease; infectious disease; allergic disease; ds.
OS Canis sp.
XX
XX Key Location/Qualifiers
FT CDS 1..990
FT /*tag= a
XX
PN JP11106350-A.
XX
PD 20-APR-1999.
XX
PP 15-MAY-1998; 98JP-0133345.
XX
PR 07-AUG-1997; 97JP-0213755.
PR 16-MAY-1997; 97JP-0127690.
XX
XX (TORA ) TORAY IND INC.
XX
XX WPI: 1999-308068/26.
XX
XX P-PSDB: AAY02339.
XX
XX A prevention and treating agent containing interleukin 12 (CxIL12) -
XX for prevention and treatment of dog and cat immune diseases
XX
XX Claim 1; Page 12; 16pp; Japanese.
XX
XX The present sequence encodes canine interleukin-12 (IL-12). The
XX specification describes a method for the prevention and treatment
XX of dog and cat immune diseases. The treatment used an agent comprising
XX dog IL-12 (CxIL12) proteins to form a heterodimer. The agent is
XX useful for preventing and treating dog and cat immune diseases,
XX including tumours, skin diseases, infectious diseases and allergic
XX diseases.
XX
XX Sequence 990 BP; 278 A; 243 C; 251 G; 218 T; 0 other:

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Query Match 60.8%; Score 972.6; DB 20; Length 990;
Best Local Similarity 99.1%; Pred. No. 1.4e-287;
Matches 978; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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```

QY 1 ATGCCCCCTGACACGACTGTGTCATCTCTGCTTTCCTGCTGCTGCTCCCTC 60
XX |||
Db 1 ATGTCACACACACGACTGTGTCATCTCTGCTTTCCTGCTGCTGCTCCCTC 60
XX |||
QY 61 ATGGCCATATGGGAATGGAGAAAGTGTATATGTTGTAGAGTGGACTGGCAACCTGAT 120
XX |||||||
Db 61 ATGGCCATATGGGAATGGAGAAAGATGTATATGTTGTAGAGTGGACTGGCAACCTGAT 120
XX |||||||
QY 121 GGGCCCGGAGAAATGCTGCTCTCACTGCGCATACCCCTGAGAAAGATGACATCACTTGG 180
XX |||||||
Db 121 GGGCCCGGAGAAATGCTGCTCTCACTGCGCATACCCCTGAGAAAGATGACATCACTTGG 180
XX |||||||
QY 181 ACCCTGAGCAGAGCAGTGAAGTCTAGGTTCTGTGTAACCTCTGACATCCAGTCCAAA 240
XX |||||||
Db 181 ACCCTGAGCAGAGCAGTGAAGTCTAGGTTCTGTGTAACCTCTGACATCCAGTCCAAA 240
XX |||||||
QY 241 GAATTTGAGATGCTGGCCAGTATACCTGCTCCATAAAGAGGCAAGGTTCTGAGCCGCTCA 300
XX |||||||
Db 241 GAATTTGAGATGCTGGCCAGTATACCTGCTCCATAAAGAGGCAAGGTTCTGAGCCGCTCA 300
XX |||||||
QY 301 CTCCTGTTGATTCACAAAAACAGATGGAATTTGCTGCACGTGATCTTAAAGAACAG 360
XX |||||||
Db 301 CTCCTGTTGATTCACAAAAACAGATGGAATTTGCTGCACGTGATCTTAAAGAACAG 360
XX |||||||
QY 361 AAAGATCCAAAAATAGATCTTTCTGAAATGTGAGGCAAGAAATTAATTTCTGACGTTTC 420
XX |||||||
Db 361 AAAGATCCAAAAATAGATCTTTCTGAAATGTGAGGCAAGAAATTAATTTCTGACGTTTC 420
XX |||||||
QY 421 ACATGCTGCTGGCTGACCGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTACAGA 480
XX |||||||
Db 421 ACATGCTGCTGGCTGACCGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTACAGA 480
XX |||||||

```

QY 481 GGCCTCTCTGACCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
|||||
Db 481 GGCTTCTCTGACCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
QY 541 AGAGTGGACAACAGGGATTTAAGAGTACACAGTGGAGTCAAGGAGGGCAGTGCCCTGC 600
|||||
Db 541 AGAGTGGACAACAGGGATTTAAGAGTACACAGTGGAGTCAAGGAGGGCAGTGCCCTGC 600
QY 601 CCCCTGCGCGAGAGAGCTACCCATCGAGGTCTGGTGGATGCTATTCAACAAGCTCAAG 660
|||||
Db 601 CCCCTGCGCGAGAGAGCTACCCATCGAGGTCTGGTGGATGCTATTCAACAAGCTCAAG 660
QY 661 TATGAAAACCTACACACAGAGCTTCTTCATCAGAGACATCATCAAAACAGACCCACA 720
|||||
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Db 961 AGCGACTGGGCACTCTGTGTCCCTGCAGT 987

Search completed: January 14, 2003, 22:26:51
Job time : 330 secs

GenCore version 5.1.3
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OH nucleic - nucleic search, using sw model

Run on: January 14, 2003, 12:09:15 : Search time 60 Seconds
(without alignments)
8172.936 Million cell updates/sec

Title: US-09-917-265-61
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Old number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	1172.4	73.3	1560	2	US-08-751-767A-11
4	983.8	61.5	990	4	US-09-079-984A-11
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6	772.6	48.3	987	1	US-08-186-529-1
7	772.6	48.3	987	1	US-08-640-386A-1
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ALIGNMENTS

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RESULT 1
US-08-751-767A-9
: Sequence 9, Application US/08751767A
: Patent No. 5994104
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: GENERAL INFORMATION:
: APPLICANT: ANDERSON, ROBERT J.
: APPLICANT: GRANT, HUGH
: APPLICANT: MACDONALD, IAN D.
: TITLE OF INVENTION: INTERLUKIN-12 FUSION PROTEIN
: NUMBER OF SEQUENCES: 80
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: NJXON & VANDERHAYE P.C.
: STREET: 1100 NORTH GLEBE ROAD
: CITY: ARLINGTON
: STATE: VA
: COUNTRY: USA
: ZIP: 22201
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/751,767A
: FILING DATE: 08-NOV-1996
: CLASSIFICATION: 536
: ATTORNEY/AGENT INFORMATION:
: NAME: SADOFF, B.J.
: REGISTRATION NUMBER: 36,663
: REFERENCE/DOCKET NUMBER: 117-221
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 7038164091
: TELEFAX: 7038164100
:
: INFORMATION FOR SEQ ID NO: 9:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1623 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..1620
:
: US-08-751-767A-9
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: Query Match 76.3%, Score 1219.4, DB 2, Length 1623:
: Best Local Similarity 85.6%, Pred. No. 0:
: Matches 1390: Conservative 0: Mismatches 206: Indels 27: Gaps 2:
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RESULT 2
US-08-751-767A-7
Sequence 7, Application US/08751767A
Patent No. 5994104
GENERAL INFORMATION:
APPLICANT: ANDERSON, ROBERT J.
APPLICANT: GRANT, HUGH
APPLICANT: MACDONALD, IAN D.
TITLE OF INVENTION: INTERLUKIN-12 FUSION PROTEIN
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentlin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08-751,767A
FILING DATE: 08-NOV-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 117-221
TELECOMMUNICATION INFORMATION:
TELEPHONE: 7038164091
TELEFAX: 7038164100
INFORMATION FOR SEQ ID NO: 7:


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: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/751,767A
: FILING DATE: 08-NOV-1996
: CLASSIFICATION: 536
: ATTORNEY/AGENT INFORMATION:
: NAME: SADOFF, B.J.
: REGISTRATION NUMBER: 36,663
: REFERENCE/DOCKET NUMBER: 117-221
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 7038164091
: TELEFAX: 7038164100
: INFORMATION FOR SEQ ID NO: 11:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1560 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..1557
: US-08-751-767A-11

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Matches 1337; Conservative 0; Mismatches 196; Indels 27; Gaps 2:

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RESULT 4
US-09-079-984A-11
: Sequence 11, Application US/09079984A
: Patent No. 6231850
: GENERAL INFORMATION:
: APPLICANT: Okano, Fumiyoshi, Satoh, Masahiro,
: APPLICANT: Yamada, Katsushige
: TITLE OF INVENTION: Canine interleukin 12, a production method
: TITLE OF INVENTION: thereof, an immune disease treatment method and preventive
: TITLE OF INVENTION: method using it

```

NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Miller & Christenbury Intellectual Property
ADDRESS: Department of Schneider, Harrison, Segal and Lewis, LLP
STREET: 1600 Market Street, 39th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,984A
FILING DATE: 15-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Austin R. Miller
REGISTRATION NUMBER: 16,602
REFERENCE/DOCKET NUMBER: 1051-98
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-1810
TELEFAX: (215) 568-6946
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 990 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Canis familiaris
FEATURE:
NAME/KEY: Canine IL12
LOCATION: 1 to 987
IDENTIFICATION METHOD: Similarity
US-09-079-984A-11

Query Match 61.5%; Score 983.8; DB 4; Length 990;
Best Local Similarity 99.8%; Pred. No. 6,8e-301;
Matches 985; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 361 AAAGATCCAAAAATTAAGATCTTTCTGAAATGTGAGCGCAAGAATATTATTCGACGTTTC 420
QY 421 ACATGCTGCTGCTGACGGCAATCAGTCAATTGAAATTCAGTCTCAAAAGTGCACAGA 480
DB 421 ACATGCTGCTGCTGACGGCAATCAGTCAATTGAAATTCAGTCTCAAAAGTGCACAGA 480

DB 421 ACATGCTGCTGCTGACGGCAATCAGTCAATTGAAATTCAGTCTCAAAAGTGCACAGA 480
QY 481 GCGTTCTCTGACCCCCCAAGGGGTGACATGTGAGCAGTACACTTTGCACAGAGGGTTC 540
DB 481 GCGTTCTCTGACCCCCCAAGGGGTGACATGTGAGCAGTACACTTTGCACAGAGGGTTC 540
QY 541 AGAGTGGACACAGGAGATTTATAGAAAGTACACAGTGGAGTGTGACAGAGGGCGTCCCTGC 600
DB 541 AGAGTGGACACAGGAGATTTATAGAAAGTACACAGTGGAGTGTGACAGAGGGCGTCCCTGC 600
QY 601 CCCCTGCGCGAGAGAGAGCTTACCCATCGAGGTGCTGCTGATGCTATTCCAAAGCTCAAG 660
DB 601 CCCCTGCGCGAGAGAGAGCTTACCCATCGAGGTGCTGCTGATGCTATTCCAAAGCTCAAG 660
QY 661 TATGAAACTACACAGCAGCTTTTTCATGACAGATCATATTAACACAGACCCACCCACA 720
DB 661 TATGAAACTACACAGCAGCTTTTTCATGACAGATCATATTAACACAGACCCACCCACA 720
QY 721 AACCTGACAGTGAAGCATTTGAAAAATCTGGCAAGTGGAGTCAAGTGGGAATTACCCC 780
DB 721 AACCTGACAGTGAAGCATTTGAAAAATCTGGCAAGTGGAGTCAAGTGGGAATTACCCC 780
QY 781 GACACCTGGAGCAGCCCAACATTCCTACTTCTCCCTGACATTTTGGATACAGGCCAGGGC 840
DB 781 GACACCTGGAGCAGCCCAACATTCCTACTTCTCCCTGACATTTTGGATACAGGCCAGGGC 840
QY 841 AAGAACATAGAGAAAGAAAGATAGACTCTGCTGAGACAGACCTCAGCCAAAGTCTGTG 900
DB 841 AAGAACATAGAGAAAGAAAGATAGACTCTGCTGAGACAGACCTCAGCCAAAGTCTGTG 900
QY 901 TGGCACAAGAGATGCCAAGATCGCGGTCGAAGCCGACAGCGGTACTATATGTTCACTCTGG 960
DB 901 TGGCACAAGAGATGCCAAGATCGCGGTCGAAGCCGACAGCGGTACTATATGTTCACTCTGG 960
QY 961 AGCGACTGGGACATCTGTTCATGCACT 987
DB 961 AGCGACTGGGACATCTGTTCATGCACT 987

RESULT 5
US-09-079-984A-1
Sequence 1, Application US/09079984A
Patent No. 6231850
GENERAL INFORMATION:
APPLICANT: Okano, Fumiyoshi, Satoh, Masahiro,
APPLICANT: Yamada, Katsushige
TITLE OF INVENTION: Canine interleukin 12, a production method
TITLE OF INVENTION: thereof, an immune disease treatment method and preventive
TITLE OF INVENTION: method using it
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Miller & Christenbury Intellectual Property
ADDRESS: Department of Schneider, Harrison, Segal and Lewis, LLP
STREET: 1600 Market Street, 39th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,984A
FILING DATE: 15-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Austin R. Miller
REGISTRATION NUMBER: 16,602
REFERENCE/DOCKET NUMBER: 1051-98
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-1810
TELEFAX: (215) 568-6946

```

: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 990 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA to mRNA
: ORIGINAL SOURCE:
: ORGANISM: Canis familiaris
: FEATURE:
: NAME/KEY: Canine IL12
: LOCATION: 1 to 987
: IDENTIFICATION METHOD: Similarity
US-09-079-984A-1

Query Match          60.6% Score 969.4: DB 4: Length 990;
Best Local Similarity 98.9% Pred. No. 2.4e-296;
Matches 976: Conservative 0: Mismatches 11: Indels 0: Gaps 0:

QY 1 ATGCACTCTGAGCAGATTGGTCATCTCCTGGTTTCCCTGCTGTTGGCGCTCCCTC 60
   1 ATGTGTACACGACGATGGTGCATCTCTGGTTTCCCTGCTGTTGGCGCTCCCTC 60
Db 1 ATGTGTACACGACGATGGTGCATCTCTGGTTTCCCTGCTGTTGGCGCTCCCTC 60

QY 61 ATGGCCATATGGGAAGTGGAGAAAGATGTTATGTTGAGAGTTGGAGTGGCACCCTGAT 120
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QY 121 GCGCCCGGAGAAATGGTGGTCCCTACCGCTGACCTGACCTGAGAAAGATGACATCTGG 180
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Db 121 GCGCCCGGAGAAATGGTGGTCCCTACCGCTGACCTGAGAAAGATGACATCTGG 180

QY 181 ACCTCAGCGCAGAGCAGTGAAGTCTAGTCTGTGTAAGTCTGACCATCAGTCAAGTCAA 240
   181 ACCTCAGCGCAGAGCAGTGAAGTCTAGTCTGTGTAAGTCTGACCATCAGTCAAGTCAA 240
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   241 GAATTTGGAGATGCTGGCAGTATACCTGCCATAAGAGGAGCAGGTTCTGAGCCCTCA 300
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QY 301 CTCCTGTTGATTACAAAGAAAGATGGAATTTGTCACCTGATATCTTAAAGGAACAG 360
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Db 301 CTCCTGTTGATTACAAAGAAAGATGGAATTTGTCACCTGATATCTTAAAGGAACAG 360

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QY 421 ACATGCTGGTGGTGGAGCGCAATGACTGATTTGAAATTCAGTGTCAAAGTAAGCAGA 480
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   661 TATGAAACTACACAGAGCTTCTTCATCAGAGACATCATCAAAACGACCCACCCACA 720
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QY 721 AACCTGAGCTGAAGCAATGTAAGAAATTTCTGAGCAGTGAAGTCAAGCTGGAAATACCCC 780
   721 AACCTGAGCTGAAGCAATGTAAGAAATTTCTGAGCAGTGAAGTCAAGCTGGAAATACCCC 780
Db 721 AACCTGAGCTGAAGCAATGTAAGAAATTTCTGAGCAGTGAAGTCAAGCTGGAAATACCCC 780

QY 781 GACACCTGGAGACCCCAATCTCTACTTCTCCCTGACATTTTGCATACAGGCCAGGGC 840
   781 GACACCTGGAGACCCCAATCTCTACTTCTCCCTGACATTTTGCATACAGGCCAGGGC 840

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Db 781 GACACCTGGAGACCCCAATCTCTACTTCTCCCTGACATTTTGCATACAGGCCAGGGC 840
QY 841 AAGAACAATAGAGAAAGAAAGATAGACTCGCTGGCAAGACCTCAGCCAGGTGCTG 900
   841 AAGAACAATAGAGAAAGAAAGATAGACTCGCTGGCAAGACCTCAGCCAGGTGCTG 900
Db 841 AAGAACAATAGAGAAAGAAAGATAGACTCGCTGGCAAGACCTCAGCCAGGTGCTG 900

QY 901 TGCCACAAGATGCCAAGATCCGGTGCAGACCCGAGACCGCTACTATGATTCCTGG 960
   901 TGCCACAAGATGCCAAGATCCGGTGCAGACCCGAGACCGCTACTATGATTCCTGG 960
Db 901 TGCCACAAGATGCCAAGATCCGGTGCAGACCCGAGACCGCTACTATGATTCCTGG 960

QY 961 AGCGACTGGGATCTGTGTATGTCAGT 987
   961 AGCGACTGGGATCTGTGTATGTCAGT 987
Db 961 AGCGACTGGGATCTGTGTATGTCAGT 987

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RESULT 6
US-08-186-529-1
: Sequence 1, Application US/08186529
: Patent No. 5573764
: GENERAL INFORMATION:
: APPLICANT: Sykes, Megan
: APPLICANT: Wolf, Stanley F.
: TITLE OF INVENTION: USE OF INTERLEUKIN-12 TO PREVENT
: TITLE OF INVENTION: GRAFT-VERSUS-HOST DISEASE
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genetics Institute, Inc., Legal Affairs
: STREET: 87 Cambridgepark Drive
: CITY: Cambridge
: STATE: MA
: COUNTRY: USA
: ZIP: 02140
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/186,529
: FILING DATE:
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: McDaniel, Patricia A.
: REGISTRATION NUMBER: 33,194
: REFERENCE/DOCKET NUMBER: GI 5225
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617-498-8401
: TELEFAX: 617-876-5851
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 987 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: ORIGINAL SOURCE:
: ORGANISM: Homo sapiens
: CELL TYPE: Lymphoblast
: CELL LINE: RPMI 8866
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..987
: US-08-186-529-1

Query Match          48.3% Score 772.6: DB 1: Length 987;
Best Local Similarity 87.1% Pred. No. 4e-234;
Matches 860: Conservative 0: Mismatches 124: Indels 3: Gaps 1:

QY 1 ATGCACTCTGAGCAGATTGGTCATCTCCTGGTTTCCCTGCTGTTGGCGCTCCCTC 60
   1 ATGCACTCTGAGCAGATTGGTCATCTCCTGGTTTCCCTGCTGTTGGCGCTCCCTC 60
Db 1 ATGCACTCTGAGCAGATTGGTCATCTCCTGGTTTCCCTGCTGTTGGCGCTCCCTC 60

QY 61 ATGGCCATATGGGAAGTGGAGAAAGATGTTATGTTGAGAGTTGGAGTGGCACCCTGAT 120
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Dh	61	GTGGGCATATGGGAAGCTAAGAAAGATCTTTATGTCGTACGATTTGGATTGGTATCCGGAT	120
QY	121	GCCTCCGAGAGAATGGTGGTCTCTCACTGCCATACCCCTGAAAGAGATGCATCACTTGG	180
Dh	121	GCCTCTGGAGAAATGGTGGTCTCTCACTGGTACACCCCTGAAGAAATGGTATCACTGG	180
QY	181	ACCTCAGCGCAGACCATTTGAAGTCTTAACTTCTGGTAAACCTTGACCATCAAGTCAA	240
Dh	181	ACCTTGGAGCTGACACATGAGAGTCTTAAAGCTTGGCAAAACCCCTGCACCATCCAAAGTC	240
QY	241	CAATTGGAGATGGCTGGCCAGTATACCTGCCATAAAGAGAGCAAGCTTTCGACCCCTCA	300
Dh	241	GAGTTTGAAGATGGCTGGCCACTACACCTGTGCACAAAGAGAGCGAGTCTTAAACCATTCG	300
QY	301	CTCCTGTTGATTCACAAAAAGAAGATGCAATTTGGTGGCTACTGATATCTTAAAGAACAC	360
Dh	301	CTCCTGGCTGCTTTCACAAAAGAAGATGCAATTTGGTGGCTACTGATATTTAAAGAACAC	360
QY	361	AAACAAATCCAAAATTAAGTCTTCTGAAATGTGACGCAAAAGAAATTAATCTGAGAGTTTC	420
Dh	361	AAAGAACCCAAAATTAAGACCTTTCTTAAGATGTGACGCGCCAAAGATTAATCTTGACGTTTC	420
QY	421	ACATCTGGTGGCTGGACGGCAATGATGACTGATTTGCAATTTGAGTGTCAAAAGTACACGA	480
Dh	421	ACCTGCTGGTGGCTGGACGACATGATGATGATTTGACATTTGACATTTGCAAAACGACACA	480
QY	481	GGCTTTCTTTGACCCCCCAAGGGGTGACATGTGGACCACTGACACTTTTCAGCAGAGAGCTC	540
Dh	481	GGCTTTCTTTGACCCCCCAAGGGGTGACGCTGGGAGACTGCTACACTCTCTCGAGAGAGATTC	540
QY	541	AGAGTGGCAGCAGCGATTAATAAAGATACACAGTGGAGTGTGAGGAGAGCGCATGGCTGG	600
Dh	541	AGAGGGGAGCAACAGAGATAT--GAGTACTCAAGTGGAGTGGCCAGAGGAGCACTGGCTGG	597
QY	601	CCCTCTGGCGAGGAGAGCCTACCCATCCAGGTCTGTGGTGAATGCTATTTCACAGCTCAAG	660
Dh	598	CCAGCTCTGGAGGAGAGCTGCCCATTTGAGTGTGATGGTATGCCGTTCCACAGCTCAAG	657
QY	661	TATGAAAGCTGACCCAGCAGCTTTCTTATACAGACATCATCAAAATTCAGCCACCCACA	720
Dh	658	TATGAAAGCTACACCAGCAGCTTCTTATACAGGACATCATCAAACTCGACCCACCAAG	717
QY	721	AACCTGCAAGCTGAGACCATTAAGAAATTTCTCGCAGCTGAGGTCAAGTGGATACCCG	780
Dh	718	AACCTGCAAGCTGAGACCATTAAGAAATTTCTCGCAGGTGAGGTCAAGTGGAGTACCTT	777
QY	781	GACACCTGGAGCACCACCATTTCTACTTCTCCCTGCATATTTGGCATACAGGCCACGGC	840
Dh	778	GACACCTGGAGTACATCCCATCTTACTTCTCCCTGCATTTGGCTTGAAGTCCGAGGC	837
QY	841	AAGAAACATTAAGAAAGAAAGATGAGACTCTGGCTGGACAAAGACTTCAGGCAAGTCTGG	900
Dh	838	AAGAGCAAGACAGAAAGAAAGATGAGTCTTACAGGACAAAGACTTCAGGCAAGTCTGG	897
QY	901	TGCCAACAAGATGCGCAGATTCGGCTCAAGCCGGAACCGCTACTACTATCTGCTGG	960
Dh	898	TGCCCAAAAATGTCACCATTTAAGGTGGGGGCCCAAGACCGCTACTATTAAGTATCTTGG	957
QY	961	AGCAGCTGGATATCTGTGTATATGCACT 987	
Dh	958	AAGCAATGGGATCTGTGGCTTGGAGT 984	

RESULT 7
 US-08-6A0-386A-1
 Sequence 1, Application US/08640386A
 Patent No. 5756085
 GENERAL INFORMATION:
 APPLICANT: Sykes, Megan
 APPLICANT: Wolf, Stanley F.
 TITLE OF INVENTION: USE OF INTERLEUKIN-12 TO PREVENT
 TITLE OF INVENTION: GRAFT-VERSUS-HOST DISEASE

```

1  NUMBER OF SEQUENCES: 4
2  CORRESPONDENCE ADDRESS:
3  ADDRESSSEE: Genetics Institute, Inc., Legal Affairs
4  STREET: 87 Cambridgepark Drive
5  CITY: Cambridge
6  STATE: MA
7  COUNTRY: USA
8  ZIP: 02140
9
10 COMPUTER READABLE FORM:
11 MEDIUM TYPE: Floppy disk
12 COMPUTER: IBM PC compatible
13 OPERATING SYSTEM: PC-DOS/MS-DOS
14 SOFTWARE: Patent Release #1.0, Version #1.25
15 CURRENT APPLICATION DATA:
16 APPLICATION NUMBER: US/08/640,386A
17 FILING DATE:
18 CLASSIFICATION: 424
19 ATTORNEY/AGENT INFORMATION:
20 NAME: Brown, Scott A.
21 REGISTRATION NUMBER: 32,724
22 REFERENCE/DOCKET NUMBER: GI 5225A
23 TELECOMMUNICATION INFORMATION:
24 TELEPHONE: 617-498-8224
25 TELEFAX: 617-876-5851
26 INFORMATION FOR SEQ ID NO: 1:
27 SEQUENCE CHARACTERISTICS:
28 LENGTH: 987 base pairs
29 TYPE: nucleic acid
30 STRANDEDNESS: single
31 TOPOLOGY: linear
32 MOLECULE TYPE: cDNA
33 ORIGINAL SOURCE:
34 ORGANISM: Homo sapiens
35 CELL TYPE: Lymphoblast
36 CELL LINE: RPMI 8866
37 FEATURE:
38 NAME/KEY: CDS
39 LOCATION: 1..987
40 US-08-640-386A-1
41
42 Query Match 48.3%; Score 772.6; DB 1; Length 987;
43 Best Local Similarity 87.1%; Pred: No. 4e-234;
44 Matches 850; Conservative 0; Mismatches 124; Indels 3; Gaps 1
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46 1 ATGCAACCCACACAGTGGTGCATCTCTGCTGTTTCCCTGTTTGGTCGCTCCCTC 60
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52 61 GTGGCCATATGAGCACTGAGAGAAGATGTTTATGTTGTAGAGTGGATTCATCGGAT 120
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54 121 GCCCGCGAGAAATGCTGCTCTCTACCTGCCATACCCCTGAAGAAGATGACATCTGG 180
55 1111111111111111111111111111111111111111111111111111111
56 121 GCCCGCGAGAAATGCTGCTCTCTACCTGCCATACCCCTGAAGAAGATGATCATCGG 180
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59 1111111111111111111111111111111111111111111111111111111
60 181 ACCCTGAGCGAGAGAGTGAAGTCTCTAGAGTCTGTGTAACACTGACATCCAGTCGAA 240
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62 241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGTTCTGAGCCGCTCA 300
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64 241 GAGTTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGTTCTGAGCCATTCG 300
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68 301 CTCCTGTGATTCACAAAAAGAGATGSAATTTGGTCCACGTGATATTTTAAAGGACAG 360
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70 361 AAAGATCAAAAATTAAGTCTTCTGGAATGTGAGCAAAAGATATATCTGAGAGTTTC 420
71 1111111111111111111111111111111111111111111111111111111
72 361 AAAGATCAAAAATTAAGTCTTCTGGAATGTGAGCAAAAGATATATCTGAGAGTTTC 420
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74 421 ACATCTCTGCTGAGCGGCAATTCAGTACTGATTTGAAATTGACGTCTCAAAAGTGCAGA 480

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Db	421	ACCTCGTGGTGGCTGACGCACATCAGTACTGATATTTGACATTTCACTGTCCAAAGCAGCAGA	480
Qy	481	GGCTTCTCTGACCCCCCAAGGGTGACATGTGGAGCAGTGCACACTTTTACGCAGAGAGGGTC	540
Db	481	GGCTTCTTCTGACCCCCCAAGGGGTGACGTGGCCGAGACTGTGTACACTCTCTGCGAGAGAGATGC	540
Qy	541	ACAGTGCACACAGGAGTATTTATAGAGTACACAGTGGAGTGTCTAGAGGGGAGTGGCTTCG	600
Db	541	AGAGGGGACACMACAGGAGTAT---GAGTACTCAGTGCAGTGTCCAGAGAGACAGTGGCTTCG	597
Qy	601	CCCTCTGCCGAGGAGAGGCTACCCATCGAGGGTCGTGTGATGCTATTTCACAGGCTCAG	660
Db	598	CCAGTGTCTGAGGAGAGTCTGGCCATCTGAGGTTCATGTGGATGCGGTTCACAAAGCTCAG	657
Qy	661	TATGAAACCTACCCAGGAGCTTCTTTCATTCAGAGCATCATCAACCAAGCCACCACA	720
Db	658	TATGAAACCTACCCAGGAGGCTTCTTTCATTCAGAGGCATCATCAACCTGACCCACCACAG	717
Qy	721	AACCTGACGCTGAAGCCATTGAAAAATTTCTGGGACGTGGAGGTCCACTGGGAATATACCC	780
Db	718	AACCTTGCAGCTGAACCCATTAAAGATTTCTGGCAGGATGGAGGTCTCAGCTGGGAGTACCTT	777
Qy	781	GACACCTGGAGCACCCACATTTCTACTTCTCCCTGCACATTTTGTCATACAGGCCACAGGC	840
Db	778	GACACCTGGAGTACTCCACATTTCTACTTCTCCCTGCACATTTTGTCATACAGGTCCAGGCG	837
Qy	841	AAGACCATATAGGAAAAAAGAAAGATATGACTGTGCTGTGCAACAAACCTTACGCCAAGTGTGC	900
Db	838	AAGACCAAGAGAGAAAAAGAAAGATATGACTTTCACGGCACAAGACCTTACGCCACGGTATC	897
Qy	901	TGCCACAAGGATGCCACAGATCCGCTGGCAAGCCCGAGACCGCTTACTATAGTTCATCCTCG	960
Db	898	TGCCCAAAAATATGCCAGCATTTAGCGTGGGGGCCCAAGGACGGCTACTATATGCTATCTTTGG	957
Qy	961	AGCGACTGGGCATCTGTGTCACTGCAGT	987
Db	958	AGCGAATGGCATCTGTGTCCCTGCAGT	984

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?                               :
? SEQUENCE CHARACTERISTICS:
? LENGTH:    1018 base pairs
? TYPE:      nucleic acid
? STRANDEDNESS: single
? TOPOLOGY:  linear
? MOLECULE TYPE:  cDNA
?
US-08-184-009-194

```

Query Match	48.3%	Score 772.6	DB 2	Length 1018
Best Local Similarity	87.1%	Pred No 4.1e-234		
Matches 860	Conservative 0	Mismatches 124	Indels 3	Gaps 1

OY	1	ATGACCCCTCGAGAGATTGGCTATCTCTGGTATTTTCCGTCGTTTGGCGGGCTCCCTC	60
Db	32	ATGTGTCACACAGCAATTTGGTCATCTCTGGTTTCCGGTTTTCGGCATCTCCCTC	91
OY	61	ATGGCATATATGGGAACCTGGAAAAAGATGTTTATGTGTAGAGTTGGACTGGCACCTGAT	120
Db	92	GTGGGCAATATGGGAACCTGAAAAAGATGTTTATGTGTAGAGTTGGATTTGATTCGGAT	151
OY	121	GGCCCCGAGAAATGTTGGTCTCTGACCTGGCCATACCCCTGGAAGAATGTGACATCACTTTGG	180
Db	132	GGCCCTGGAGAAATGTTGGTCTCTGACCTGTGACACCCCTGGAAGAATGTGATTCACCTGG	211
OY	181	ACCTCAGCGCAGAGCACTGGAAGTCTTAGTTCGTGTAACCTGTGACCATTCCAAAGTCAAA	240
Db	212	ACCTTGGACACGAGACAGTAGAGTCTTAGGCTCTGGCAAAACCCGTGACATTCACAGTCAAA	271
OY	241	GAATTTGGAGATGTCGGGCAGTATACCTGGCATTAAGAGGCAAGGTTTGGAGGCGCTCA	300
Db	272	GAGTTTGGAGATGCTGGCCAGTATACCTGTGACAAAGAGGCGAGGTTCTTAAGCATTTGG	331
OY	301	CTCCTGTTGATTTCAACAAAAAAGAGATGGAATTTAGTGTGCTACACTGATATCTTAAAGAACAG	360
Db	332	CTCCTGCTGTTTCAACAAAAAAGAGATGGAATTTAGTGTGCTACATGATATTTTAAAGGACAG	391
OY	361	AAAGATATCCAAAAATAGATCTTTCTGAAATGTGAGCCAAAGAATTTATTGCAAGCTTTG	420
Db	392	AAAGAACCCCAAAATATAGACCTTTCTTAAGATGCGAGGCGCAAGAAATTTCTGCGACGTTTC	451
OY	421	ACATCTCTGGTGGCGACGGCAGTACGTATCTAATTTGAAATTCAGTGTCAAAAGATGAGA	480
Db	452	ACCTGCTGGTGGCGTGGACGACATCACTAATTTTGACATTTCAAGTGTCAAAAGAGCAGAGA	511
OY	481	GACTTCTCTGACCCCCCAAGGGGTGACATGTGGAGCACTGACACTTTTGACGAGAGAGGTC	540
Db	512	GGCTTCTCTGACCCCCCAAGGGGTGACGTCGGAGACTCTCTACACTCTCTGCAAGAGAGTC	571
OY	541	AGAGTGGCACACAGGATATTAAAGATGACACACTGTGGAGTGTGAGAGGGCAGTGCCTGC	600
Db	572	AGAGGGGACAACAAGGAATAT--GAGTACTCACTGGAGTGTGCCGAGGAGCAGTGCCTGC	628
OY	601	CCCTTGTGCGAGGAGAGCTTACCATTGGAGGTGCTGGTGTGATTTATTCACAAAGCTAAG	650
Db	629	CCAGTGTGTGAGGAGAGTCTGCCCATTTGAGGTGATGTGGATGGCGTTTCAACAAAGCTAAG	688
OY	651	TATGAAACATCACACGACGCTTCTTATCATCAGACATCATCAAACGACCAACCCACA	720
Db	689	TATGAAACATCACACGACGCTTCTTATCATCAGGACATCATCAAACCTGACCCCAACG	748
OY	721	AACCGGAGCGTGAAGCCATTGAAAAATTTCTGCGAGCTGGAGGTGCACTGGGAAATACCC	780
Db	749	AACCTTGACGCTGAAGCCATTGAAAAATTTCTGCGAGGTGAGAGGTGCACTGGGAGTACCTT	808
OY	781	GACACCTGGACACCCCACTTCTACTTTCCTCTGACATTTTGCATTAAGGCCACAGGC	840
Db	809	GACACCTGGAGTACTTCCACATCTCTACTTCTTCCCTGACATTTCTGCTTACAGTGTCAAGGC	868
OY	841	AAGAACATAGACAAAAAAGATAGACTCTGCGTGGACAAGACCTTCAGCCGAAGTCTG	900
Db	869	AAGGACAAGAGAAAAAGATAGAGTCTTTCACGGAACAAAGACTTCAGCCAGGCTATC	928

Cl	Sequence	Position
Cl	901 TGTACGACGATGGCCAGATCCGGGCTGTAACGCCAGACGCTACATATACATTCCTGG	960
	1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111	
D3	929 TGGCCAAATAATGCCAGATTAGCTGTGGGGGCTAGAACCCCTGACTATAGCTCATCTTGG	988
Cl	961 AGCGACTGGGCATCTGTCTCATTCGACT	987
	1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111	
D3	989 AGCGAATGGGCATCTGTCTCATTCGACT	1015

RESULTS

US-08-458-194
Sequence 194, Application US/08458195
Patent No. 5942235
GENERAL INFORMATION:
APPLICANT: Proietti, Enzo
APPLICANT: Taradella, James
APPLICANT: Cox, William I.
TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
NUMBER OF SEQUENCES: 217
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford
STREET: 530 Fifth Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,356
FILING DATE: 02-JUN-1995
CLASSIFICATION: A24
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/184,009
FILING DATE: 19-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454110-2530
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
TELEX: 425056COURTMS
INFORMATION FOR SEQ ID NO: 194:
SEQUENCE CHARACTERISTICS:
LENGTH: 1018 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-458-356-194

Query Match 48.38; Score 772.6; DB 2; Length 1018;

Best Local Similarity 87.1%; Pred. NO. 4.1e-234;
Matches 860; Conservative 0; Mismatches 124; Indels 3; Gaps 1;

QY	1	ATGGACCCCTGACAGATTGGTCAATCCCTGGATTTCCTCGTTGGTGGTGTCTCCGCTC	60
Db	32	ATGTGTCAAGCAGAGATTGGTATCTCTTGGATTTTCCTCGTTTTCGTGGATCTCCCTCTC	91
QY	61	ATGGGCATATGGGAACCTGGAGAAAGATGTTATGTTGTAGACATTGACCTGGACCCGTAT	120
Db	92	GTGGGCGCATATGGCAATCGAAGAAAGATGTTATGTGTCTGACATTTGCAATTTGGTATCCGAT	151
QY	121	GGCCCCGGAGAAATGTTGGTCTCTCAAGCTGCACATACCCCTGAGAGAAGATGCATTCACCTGG	180
Db	152	GGCCCTTGAGAAATGTGTGTGTCTCTCAACCTGTAGACACCCCTGAAAGAAATGGTATTCACCTGG	211
QY	181	ACCTTCAGCGCAGAGACCACTGAAGTCTTGAGTTCTGTGTAAGACTCTGACCAATCCGAAGTCAAA	240

Dh	212	ACCTTTGGACACGAGAGAGTGGAGGTCTTTAGGCTCTGGCAAAACCTGACCATTCGAAGTCAAA	2711
QY	241	GAATTTTGGAGATGCTGGCCACTATTACCTGCCATTAAGGAGGCAAGTTCTGAGCCGCTCA	3000
Dh	272	GAGTTTGGAGATGCTGGCCACTTACCGCTGCACAAAGAGGCGGAGTTCTTAAGCATTTGC	3313
OY	301	CTCCGTGTTGATTTCACAAAAGAAGATGGAAATTGGTCTGCTGATATCTTAATAAGAACAG	3660
Dh	332	CTTCCTCGCTGCTTCACAAAAGAAGATGGAAATTGGTCTGCTGATATTTTAAAGGACAC	3911
QY	361	AAAGATTCACAAAATTAAGATCTTCTGTAATGATGAGCCAAAAGATTTATTCTGGACGTTTC	4200
Dh	392	AAAGACACCCAAAATTAAGACCTTTCTTAAGATGCGAGGCCAAGATTTATTCTGGACGTTTC	4511
QY	421	ACATTCCTGGTGGCTGACGGCAATCAGTACTGATTTTGAATTTCACTGTCAAAAAGTACGAGA	4800
Dh	452	ACCTTCCTGGTGGCTGACGACCAATCAGTACTGATTTTGAATTTCACTGTCTCAAAAAGCAGAGA	5111
QY	481	GCGTTCTCTTGACCCCCAAGGGGTGACATGTGGAGCACTTGACATTTTACGACGAGAGGTC	5400
Dh	512	GCGTTCTCTTGACCCCCAAGGGGTGACGCGCGAGCTGCTACACTCTCTGCGACGAGAGGTC	5711
QY	541	AGACGTGGCACACGGGATTTAACAAGTACACACTGGAGTCTCGAGGAGGGAGTGCCTGC	6000
Dh	572	AGAGGGGACACACAGGATAT--GAGTACTCAGTGGAGTCCGAGGAGACAGTGCCTGC	6280
QY	601	CCCTTGTCCGAGGAGAGCTACCCATCGAGGTGCTGGTGATCTATTTCACAAAGCTCAAG	6600
Dh	629	CCAGCTGCTGGAGGAGAGTCTGCCATTGTAGGTGATGTTGCCGTTTCACAAAGCTCAAG	6880
QY	661	TATGCAAAATCTACACGACGAGCTTCTCATCGAGACATCATCAAAAGCAGACCCACCA	7200
QY	721	AACCTGCAAGCTGAAGCCATTGAAAAATTTCTGGGACGTGGAGTCTACCTGGGAATPACCC	7800
Dh	749	AACCTGCAAGCTGAAGCCATTGAAAAATTTCTGGGACGTGGAGTCTACCTGGGAATPACCT	8080
QY	781	GACACCTGGACACCCCATTTCTTACTTCTCCCTGACATTTTGCATACAGGCCACGAGG	8400
Dh	809	GACACCTGGAGTACTCCGACATTCTACTTCTTCCCTGACATTTCTGCTTCAGGTCCAGGGC	8680
QY	841	AAGAACTAATTAAGAAAAGAAAGATAGACTCTGCTGGACAGACAGACTGAGCCAAAGTCGTG	9000
Dh	869	AAGAACTAATTAAGAAAAGAAAGATAGAGTCTTTCACGGGCAAGACCTGAGCCAGCGTCATC	9280
QY	901	TGCCCAAGGATGCCAGATCCGCTGCAAGCCCGAGACCGCTACTATTAGTTACTCTGG	9600
Dh	929	TGCCCAAAATTAAGCAATTAGCGTGGGCGCCGAGGACCGCTACTATTAGTCTACTTTGG	9880
QY	961	AGCGACTTGGGATCTGTTCTCATCTGAGT	987
Dh	989	AGCGAATGCGCATCTGTGCTCCCTGACAGT	1015

RESULT 10

US-08-460-736-194
; Sequence 194, Application US/08460736

```

1  GENERAL INFORMATION:
2  APPLICANT:  Paoletti, Enzo
3  APPLICANT:  Tartaglia, James
4  APPLICANT:  Cox, William I.
5  TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
6  NUMBER OF SEQUENCES:  217
7  CORRESPONDENCE ADDRESS:
8  ADDRESSEE:  Curtiss, Morris & Safford
9  STREET:  530 Fifth Avenue
10 CITY:  New York
11 STATE:  NY
12 COUNTRY:  USA
13 ZIP:  110036

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460.736
FILING DATE: 02-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/184,009
FILING DATE: 19-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2530
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
TELEX: 425066CURPMS
INFORMATION FOR SEQ ID NO: 194:
SEQUENCE CHARACTERISTICS:
LENGTH: 1018 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-460-736-194

Query Match 48.3% Score 772.6; DB 4; Length 1018;
Best Local Similarity 87.1%; Pred. No. 4; Le-234;
Matches 860; Conservative 0; Mismatches 124; Indels 3; Gaps 1;

QY 1 ATGCACCTCTGACGATGTCATCTCTCTGCTGTTTCCCTGCTTTCCTGCGCTCCCTC 60
DB 32 ATGTGTACACGACGATGTGTCTCTCTGTTTCCCTGCTTTCCTGCGATCTCCCTC 91
QY 61 ATGGCCATATGGAAGCTGGAAGAGATGTTATGTTGATAGTTGGACTGGCACCCCTAT 120
DB 92 GTGGCATATGGAAGCTGGAAGAGATGTTATGTTGATAGTTGGATGGATCCGAT 151
QY 121 GCGCCGGAAGAAATGCTGCTCTCCTGCTCCATACCCCTGAAGAAGATGACATCTGG 180
DB 152 GCGCCCTGGAAGAAATGCTGCTCTCCTGCTCCATACCCCTGAAGAAGATGATACCTG 211
QY 181 ACCTCAGCGGAGAGAGATGGAAGTCTAGCTTCTGTTAAAGCTGACCATCCAGTCAAA 240
DB 212 ACCTTTGACGACGAGAGAGTGTAGGCTCTGCAAAAACCTGACCATCCAGTCAAA 271
QY 241 GAATTTGAGATGCTGCGCAGTATACCTGCAATGAAGAGGCAAGCTTCTGAGCCGCTCA 300
DB 272 GAGTTTGAAGATGCTGCGCAGTATACCTGCAATGAAGAGGAGGCTTCTGAAGCATTCG 331
QY 301 CTCTGTTGATTCACAAAAGAGATGGAATTTGTTGCTCATGATATCTTAAAGAAACAG 360
DB 332 CTCTGCTGCTTCAAAAAGAGATGGAATTTGTTGCTCATGATATCTTAAAGAAACAG 391
QY 361 AAGAATTCAAAATTAAGATCTTCTGAATGTGAGCAAGAATTAATTCAGAGGCTTC 420
DB 392 AAGAATTCAAAATTAAGATCTTCTGAATGTGAGCAAGAATTAATTCAGAGGCTTC 451
QY 421 ACATGCTGCTGCTGAGCGCATCTAGTATGTTGAATTCAGTGTCAAAAGTAGCAGA 480
DB 452 ACCTGCTGCTGCTGAGCAGCATCTAGTATGTTGAATTCAGTGTCAAAAGTAGCAGA 511
QY 481 GCGTTCCTGACCCGCAAGGGGTGACATGTGGAGCAGTCACTTTCAAGCAGAGGCTC 540
DB 512 GCGTTCCTGACCCGCAAGGGGTGACATGTGGAGCAGTCACTTTCAAGCAGAGGCTC 571
QY 541 AGACTGACACAGGATTAAGAAGTACAGAGTGAAGTGAAGTGAAGGAGAGGAGGCTGC 600
DB 572 AGAGGGGACACAGAGGATTAAGAAGTGAAGTGAAGTGAAGGAGAGGAGGAGGCTGC 628

QY 601 CCCTCTGCGGAGAGAGCCCTACCATCGAGTGTGATGCTATTCACAAAGCTCAAG 660
DB 629 CCAGCTCTGAGAGAGAGTCTGGCCATTTAGGTCATGATGATGCCGTTACAGAGTCAAG 688
QY 661 TATGAANAATACACAGAGCTTCTTCATCAGAGCATCATCAAAACAGACCCACCCACA 720
DB 689 TATGAANAATACACAGAGCTTCTTCATCAGAGCATCATCAAAACAGACCCACCCACA 748
QY 721 AACCTGCAAGTGAAGCCATTTGAAAATTCGGCGAGGAGGAGGAGTGGGAATATCCC 780
DB 749 AACCTGCAAGTGAAGCCATTTGAAAATTCGGCGAGGAGGAGTGGGAATATCCC 808
QY 781 GACACCTGAGACACCCACATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 840
DB 809 GACACCTGAGTACCTCCACATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 868
QY 841 AAGAACAATAGAAAGAAAGATAGACTCTGCTGGAACAAGACTGACCAAGTGTG 900
DB 869 AAGACCAAGAGAGAAAGAAAGATAGACTCTGCTGGAACAAGACTGACCAAGTGTG 928
QY 901 TGCCCAAGAGATGCCAAGATCGCGGTGCAAGCCGAGACCGCTATATATTCATCTCTG 960
DB 929 TGCCCAAGAAATGCCAAGATTCAGGCTGCGGCGCCAGAGACCGCTATATATTCATCT 988
QY 961 AGCGACTGGCATCTGTCTCATGTCAGT 987
DB 989 AGCGAATGGCATCTGTCTCTCTGTCAGT 1015

RESULT 11
US-08-751-767A-3
Sequence 3, Application US/08751767A
Patent No. 5994104

GENERAL INFORMATION:

APPLICANT: ANDERSON, ROBERT J.

APPLICANT: GRANT, HUGH

APPLICANT: MACDONALD, IAN D.

TITLE OF INVENTION: INTERLUKIN-12 FUSION PROTEIN

NUMBER OF SEQUENCES: 80

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHIE P.C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VA

COUNTRY: USA

ZIP: 22201

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/751,767A

FILING DATE: 08-NOV-1996

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: SADOFF, B. J.

REGISTRATION NUMBER: 36,663

REFERENCE/DOCKET NUMBER: 117-221

TELECOMMUNICATION INFORMATION:

TELEPHONE: 7038164091

TELEFAX: 7038164100

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 1399 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 43..1026

US-08-751-767A-3


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0Y 301 CTCCTGTTGATTTCACAAAAAAGAGATGCAATTTTGGTCCACTGATTCCTAAAGGAACAG 360
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 333 CTCCTGCTGCTTTCACAAAAAAGAGATGGAATTTTGGTCCACTGATTCCTAAAGGAACAG 332
0Y 361 AAGAATTCACAAAAATAGATCTTCTGCAATGTGAGGCAAAAGATTAATTCCTGAGCTTTTC 420
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 393 AAGAATACCCAAAAAATAGACCTTTTCTAAGATGCGAGGCAAAAGATTAATTCCTGAGCTTTTC 452
0Y 421 ACATCTGCTGCTGCTGAGGCAATGATCTGATTTTGAATTCAGTGTCAAAAGTAGACAGA 480
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 453 ACCTGCTGCTGCTGCTGACACATCAGTACGATTTTGAACATTCAGTGTCAAAAGTAGACAGA 512
0Y 481 GCTTCTGACCCCCCAAGGGGGTGCATGTTGAGACACAGACATTTGAGAGAGAGGTC 540
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 513 GCTCTTTTGTGACCCCCAAGGGGGTGCATGTTGAGACACAGACATTTGAGAGAGAGGTC 572
0Y 541 AGAGTGGACAACAGGAGATTAATAGAGAGTACACACTGAGAGTGTGACGAGAGGCACTGCTGC 600
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 573 AGAGGGGACAACAGAGAGTAT--GACTACTCAGTGGAGTGTCCAGAGAGAGACACTGCTGC 629
0Y 601 CCCTTGTCCGAGAGAGGCTTACCCATGAGAGTGTGTGTGATGCTAATTCACAAGTTCAG 650
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 630 CCAGCTGCTGAGAGAGTCTGCCCAATTGAGGCTCATGGTGGATGCGCTTCAACAAGCTCAAG 689
0Y 661 TATGAAACTACACAGAGGCTTCTTCATCAGACATTCATCAAAACCAAGCCACCCACACA 720
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 690 TATGAAAACTACCCAGAGGCTTCTTCATCAGGAGCATCATCAAACTGAGCCACCCACAG 749
0Y 721 AACCTGACGCTGAAGCCATTGAAAAAATTCCTGCGACCTGAGAGGCTGAGCTGGAAATACCC 780
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 750 AACCTGACGCTGAAGCCATTGAAAAAATTCCTGCGACCTGAGAGGCTGAGCTGGAAATACCC 809
0Y 781 GACACTTGAGACACCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCACAGGGC 840
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Db 810 GACACTTGAGTACTCCACATTCCTACTTCTCCCTGACATTTTGCCTTCCAGTCCAGGCCAGGGC 869
0Y 841 AAGAATCATACAGAAAAAAGAAATAGACTCTGCTGGACAAAGACTTAGCCAGAGTCTGTG 900
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 870 AAGAGCAAGACAGAAAAAAGAAATAGAGTCTTCAAGGACAAGACTTAGCCAGAGTCTGTG 929
0Y 901 TGCCACAAGAGTGGCAAGATCCGCTGCAAGCCCGAGAACCGCTACTTACTTACTCTCTGG 960
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 930 TGCCGCAAAAATGGCAGGATTAAGGCTGCGGGCCAGAGACCGCTACTTACTTACTCTGTGG 989
0Y 961 AGCGACTGGGCATCTGTCTCATGTCAGT 987
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 990 AGCGAATGGCATCTGTGCTCTGTCAGT 1016

SUBT 13
US-08-621-493-1
; Sequence 1, Application US/08621493
; Patent No. 5723127
; GENERAL INFORMATION:
; APPLICANT: Scott, Phillip
; APPLICANT: Trinchieri, Giorgio
; TITLE OF INVENTION: Compositions and Methods for Use of
; TITLE OF INVENTION: IL-12 as an Adjuvant
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Center, PO Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621 493

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	PILING DATE:	25-MAR-1996
:	CLASSIFICATION:	424
:	PRIOR APPLICATION DATA:	
:	APPLICATION NUMBER:	08/265,087
:	FILING DATE:	17-JUN-1994
:	APPLICATION NUMBER:	US 08/229,282
:	FILING DATE:	18-APR-1994
:	ATTORNEY/AGENT INFORMATION:	
:	NAME:	Bak, Mary E.
:	REGISTRATION NUMBER:	31,215
:	REFERENCE/DOCKET NUMBER:	WTSJLAUSA
:	TELECOMMUNICATION INFORMATION:	
:	TELEPHONE:	215-540-9206
:	TELEFAX:	215-540-5818
:	INFORMATION FOR SEQ ID NO: 1:	
:	SEQUENCE CHARACTERISTICS:	
:	LENGTH:	2362 base pairs
:	TYPE:	nucleic acid
:	STRANDEDNESS:	double
:	TOPOLOGY:	unknown
:	MOLECULE TYPE:	cDNA
:	FEATURE:	
:	NAME/KEY:	CDS
:	LOCATION:	33..1016
:	US-08-621-493-1	
<hr/>		
Query Match	48.3%	Score 772.6; DB 1; Length 2362;
Best Local Similarity	87.1%;	Pred. No. 6,7e+234;
Matches 860; Conservative 0; Mismatches 124; Indels 3; Gaps 1;		
QY	1	ATGCACCTTCAGCACTGGTGTGATCTCTCGTGTTTCCCTCGTTTTGCTGGCGTCTCCCTC 60
Dp	33	ATGTGTACACAGCACACTTGTGATCTCTGTTTCCCTCGTTTTGCTGGCATCTCCCTC 92
OY	61	ATGGCATATATGGAACTGAGAAAGATGTTATGTTGTAAGTAGTGGACCTGCAT 120
Dp	93	GTCGCCATATATGGAACTGAAGAAGATGTTATGTCGTGAATTTGGATTGATCCGAT 152
OY	121	GCCTCCGAGAAATGGTGGTCTCCACCCTGCCATACCCTCGAAGAAGATGACATCTGG 180
Dp	153	GCCTCCGAGAAATGGTGGTCTCCACCCTGCCATACCCTCGAAGAAGATGATGATCACTGG 212
OY	181	ACCTGACGGCGAGAGCAGTGAAGTCTTACGTTCTGGTAAAACCTCTACCATCCAAGTCANA 240
Dp	213	ACCTTGGACACGAGCAGTGAAGTCTTACGTTCTGGTAAAACCTCTACCATCCAAGTCANA 272
OY	241	GAATTTGAGATGTGGCCAGTATACCTGCCATAAAGGAGCGCAAGGTTGTGACGGCTCA 300
Dp	273	GAGTTTGGAGATGCTGGCCAGTACACTGTCACAAGAAGGCGAGGTTCTAAGCCATTGG 332
OY	301	CTCTGTTGATTTCACAAAAAAGAAAGATGGAATTTGGTCCACTGATATCTTAAAGGAAGAG 360
Dp	333	CTCTGTTGATTTCACAAAAAAGAAAGATGGAATTTGGTCCACTGATATTTTAAAGGAAGAG 392
OY	361	AAAGAATCCAAAATATAGATCTTTTGTGAATGTGACGCAAGAAGATTTATTTGAGCGTTTC 420
Dp	393	AAAGAATCCAAAATATAGATCTTTTGTGAATGTGACGCGCAAGAAGATTTATTTGAGCGTTTC 452
OY	421	ACATGCTGGTGGCTGACGGCAATCGTACTGTATTTGAATAATTCAGTGTCAAAGTGAAGCA 480
Dp	453	ACCTGCTGGTGGCTGACGAATCTGATCTGATTTTGAATTCAGTGTCAAAGTGAAGCA 512
OY	481	GAGCTTCGTGACCCCAAGAGGGGTGATGTTGAGCAGTACACTTTCAGCAGAGAGGGTC 540
Dp	513	GAGCTTCGTGACCCCAAGAGGGGTGATGTTGAGCAGTACACTTTCAGCAGAGAGAGTC 572
OY	541	AGAGTGGACAACAGGATTTAAGAAGTACACAGTGAAGTGTGACGAGGAGGCAAGTCCCTGC 600
Dp	573	AGAGTGGACAACAGGATTTAAGAAGTACACAGTGAAGTGTGACGAGGAGGCAAGTCCCTGC 629
OY	601	CCCTCTGTGCGGAGAGAGCTTACCATCGAGGTCGTGGTGGATGCTTATTTACACAAGCTCAAG 660
Dp	630	CCAGCTGTGAGAGAGTCTCCCATTTGAGTCAATGCTGATGCGGTTCCCTACAAAGCTTCAAG 689

cy	661	TATGAAAGCTACCCAGAGGCTCTTCATGAGAACATCATCAAGCCAGGCCAGCA	720
pb	650	TATGAAAGCTACCCAGAGGCTCTTCATGAGAACATCATCAAGCCAGGCCAG	719
cy	721	AACCGCATCTGAAGCCATTGAGAAATTTCTGGGACGCTGAGAGGTGACGTGGAAATACCCG	780
pb	720	AACCTGCAGACTGAAGCATTTAAAGATTTCTGGGACGCTGGAGTGGAGTACCT	809
cy	781	GACACCTGGAGACCCGACATTTCTACTCTCTCCCTGCACATTTTGCATACAGGCCAAGGC	840
pb	810	GACACCTGGACTATCTGCACATTTCTACTCTCTCCCTGCACATTTTCCGTTTCAAGTCCAGGC	869
cy	811	AAGAGCATACAGAAAGAAAGATAGACCTCTGGCTGACAAAGACCTTAGCCAAAGTCTG	900
pb	870	AAGAGCATAGAGAAAGAAAGATAGAGCTTTTACCGAAGAAAGCTCAGCCAGCTATC	929
cy	901	TGCCAAGAGGTGCCAAGATCCGGCTGTGCAAAGCCGAGACGCTACGTACGTATCTCTG	960
pb	930	TGCCCAAAATATGCCAGACATTAGCGTTTGGGCCGACAGAGCCGCTACGTATACCTCATCTTG	989
cy	961	AAGCAGCTGGGCATCTGTGTCTATTCAGT	987
pb	950	AGCCGATGGGCATTTGTGCCCTGCAGT	1016

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RESULT 14-588-1
US-08-965-688-1
Sequence 1, Application US/08965688
Patent No. 5976539
GENERAL INFORMATION:
APPLICANT: Scott, Phillip
APPLICANT: Trinchieri, Giorgio
TITLE OF INVENTION: Compositions and Methods for Use of
TITLE OF INVENTION: 11-12 as an Adjuvant
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Center, PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 15477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/965,688
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/621,453
FILING DATE: 25-MAR-1995
APPLICATION NUMBER: 08/265,067
FILING DATE: 17-JUN-1994
APPLICATION NUMBER: US 08/229,282
FILING DATE: 18-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/PACKET NUMBER: W5151AUSA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9206
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2362 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA

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;      FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  33..1016
US-08-965-688-1

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Query Match	48.3%	Score 772.6;	DB 2;	Length 2362;
Best Local Similarity	87.1%;	Pred. No. 6.7e-234;		
Matches 860;	Conservative 0;	Mismatches 124;	Indels 3;	Gaps 1

OY	1	ATTCACCCCTGCAGAGATTGGCATCCGATCCCGGATTTTCCCGCTGGTTGGAGGCTCCGCCCTC	60
Db	33	ATGTGTGCACCGACGACTGGTGTATCTCTTTGGTTTCCCGTGGTTTCTTGTGGCATCTCCGCCCTC	92
OY	61	ATGGCCATATATGGAACTGGAGAAAGATGTTATGTGTAGAGTTGGACTGGACCCCTGAT	120
Db	93	GTGGCCATATATGGAACTGAAGAAAGATGTATTATGTGCGAGAAATTGGATTGGTATCCGGAT	152
OY	121	GCCCCCGGAGAAATGTGTGTCTCACTGACCTGGCATACCCCTGAAGAAGATGACATCACTTGG	180
Db	153	GCCCCCGGAGAAATGTGTGTCTCACTGACACCCCTGAAGAAGATGTGATATCCCTGG	212
OY	181	ACCTTGAGGGCAGAGACAGTGAAGTCCCTAGGTTCTGGTAAACCTTGACCACATCCAGTCAAA	240
Db	213	ACCTTTGGACCGACAGAGTGAAGTCTTAGGCTCTGGCAAAACCCCTGACACATCAAGTCAAA	272
OY	241	GAATTGGAGAGATGCTGGCGACGATATACCTGGCCATTAAGAGAGCAAGTTCGTGAGCCGCTCA	300
Db	273	GAGTTTGGAGATGCTGGCGACGATATACCGCTGCACAAAGAGGCGAGGTCTTAAGCATTTGG	332
OY	301	CTTCTGTTTGATTTCACAAAAAAGAAATGGAAATTTTGGTCACTGATATCTTTAAAGCAACAG	360
Db	333	CTTCTGCTGGCTTTCACAAAAAAGAAATGGAAATTTTGGTCACTGATATTTTAAAGGACACAG	392
OY	361	AAAGATATCCAAAAATTAACATCTTCTGTGAATGTGAGCAAGGCAAAATTTATTCGTGACGTTTC	420
Db	393	AAAGATATCCAAAAATTAAGACTCTTCTTAAGATGTGCAAGGCAAAATTTATTCGTGACGTTTC	452
OY	421	ACATGCTGGTGGGCTGACGGCAATCACTACTATTTGAAATTCACGTGTCAAAGATGACAGA	480
Db	453	ACCTGCTGGTGGGCTGACCAATCACTACTATTTGAAATTCACGTGTCAAAGATGACAGA	512
OY	481	GGCCTTCTGTGACCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCACGACAGAGGGTC	540
Db	513	GGCCTTCTGTGACCCCAAGGGGTGACGCGGAGACTGCTACACTCTCTCGAGAGAGAGTC	572
OY	541	AGAGTGGGACCAACAGGATTTAAGAGATACACAGTGGAGTCTGACGAGAGGAGAGTGGCTGC	600
Db	573	AGAGGCGCAACCAAGGATTAAT--GAGTACTGAGTGGAGTCCGAGGAGGAGAGTGGCTGC	628
OY	601	CCCTTCGCGAGAGAGAGCTTACCATCGAGTGTGGTGGATGCTATTTCACAACTCAAG	660
Db	630	CCAGCTGTGTGAGAGAGTCTGCCATTTGAGGTCAATGTGGATGGCGTTTCACAAAGTCAAG	688
OY	661	TATCAAAACCTACACCAGCAGCTTCTTCATCAGAGACATCATCAAAAGACAGACCCACCCACA	720
Db	690	TATGAAACCTACACCAGCAGCTTCTTCATCAGGACATCATCAAACTGAACCCACCCACAG	748
OY	721	AACCTGCAAGCTGAAGCCATTGAAAAATTTCTGGGACGCTGGAGGTGACCTGGGAAATACCC	780
Db	750	AACCTGCAAGCTGAAGCCATTGAAAAATTTCTGGGAGGTGACCTGGGAAATATCCCT	808
OY	781	GACACCTGTGACACCCCATTTCTTACTTCCCTGTGACATTTTGCATACAGGCCCAAGGC	840
Db	810	GACACCTGTGAGTACTCCACATCTCTACTTCTCCTGTGACATTTTGCATACAGGTCCAGGCC	868
OY	841	AAGAACAATAGAGAAAAGAAAGATAGACTGTGCTGTGAGCAAGAGACTTCAGCCAAAGTTCGTG	900
Db	870	AAGAGCAAGAGAGAAAAGAAAGATAGAGTCTTTCACGGAACAAGACTTCAGCCAAAGTTCATC	928
OY	901	TGCCACAAGGATGCGCAGATTCGGCGTGTGCAAGGCCGAGACCGCTACTATAGTTACTCTGTG	960
Db	930	TGCCCCCAAAAATTTGGCAGATTAGGCTGTGGGGCCGAGGACCGCTACTATAGTTACTCTGTG	988


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Db 181 ACCGACGGCAGACAGGAGTCTAGTCTGTGTAACCTGACCATCCAAAGTCAA 240
Oy 241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATTAAGGAGGCAAGTTCTGAGCGGCTCA 300
Db 241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATTAAGGAGGCAAGTTCTGAGCGGCTCA 300
Oy 301 CTCCTGTTGATTCACAAAAAAGAGATGGAATTTGGTCCACTGATATCTTAAAGAACAG 360
Db 301 CTCCTGTTGATTCACAAAAAAGAGATGGAATTTGGTCCACTGATATCTTAAAGAACAG 360
Oy 361 AAAAATCCAAAAATAGATCTTTCTGAAATGTGAGGCAAAAGATTTCTTGACGTTTC 420
Db 361 AAAAATCCAAAAATAGATCTTTCTGAAATGTGAGGCAAAAGATTTCTTGACGTTTC 420
Oy 421 ACATGCTGGTGGTGTAGCGGCATCAGTATGTTGAAATTCAGTGCACAAAGTAGCAGA 480
Db 421 ACATGCTGGTGGTGTAGCGGCATCAGTATGTTGAAATTCAGTGCACAAAGTAGCAGA 480
Oy 481 GGCCTCTCTGACCCCAAGGGGTGACATGTGAGCAGCAGTTCAGCAGAGAGGGTC 540
Db 481 GGCCTCTCTGACCCCAAGGGGTGACATGTGAGCAGCAGTTCAGCAGAGAGGGTC 540
Oy 541 AGATGTGACACAGGAGTATTAAGACGTACACAGTGGAGTGTACAGAGGGCAGTCCTC 600
Db 541 AGATGTGACACAGGAGTATTAAGACGTACACAGTGGAGTGTACAGAGGGCAGTCCTC 600
Oy 601 CCCCTGCGGAGAGAGAGCTACCCATCGAGGTGTGTGATGCTATTCACAACTCAAG 660
Db 601 CCCCTGCGGAGAGAGAGCTACCCATCGAGGTGTGTGATGCTATTCACAACTCAAG 660
Oy 661 TATTAANAATACACAGAGCTTCTTATCAGAGACATCAACAGACCCACCACA 720
Db 661 TATTAANAATACACAGAGCTTCTTATCAGAGACATCAACAGACCCACCACA 720
Oy 721 AACCTGAGCTGAAGCCATTGAATAATCTCGGCACGTGAGGTGACGTGGAAATACCCC 780
Db 721 AACCTGAGCTGAAGCCATTGAATAATCTCGGCACGTGAGGTGACGTGGAAATACCCC 780
Oy 781 GACACCTGGAGACACCCACATCTCTACTTCTCCTGACATTTTGCATACAGGCCAGGGC 840
Db 781 GACACCTGGAGACACCCACATCTCTACTTCTCCTGACATTTTGCATACAGGCCAGGGC 840
Oy 841 AAGAACAATAGAGAAAGAAAGATAGACTGTGCTGCAAGACACTCAGCCAAAGTGTG 900
Db 841 AAGAACAATAGAGAAAGAAAGATAGACTGTGCTGCAAGACACTCAGCCAAAGTGTG 900
Oy 901 TGCCACAAGGATGGCAGATCCGGGTGCAAGCCGAGACCGCTTACTATAGTTCAATCCGG 960
Db 901 TGCCACAAGGATGGCAGATCCGGGTGCAAGCCGAGACCGCTTACTATAGTTCAATCCGG 960
Oy 961 AGGACCTGGGCATCTGTGTATGAGTGTGCGGTGGCGGGCGGATAGAAACTTGGCA 1020
Db 961 AGGACCTGGGCATCTGTGTATGAGTGTGCGGTGGCGGGCGGATAGAAACTTGGCA 1020
Oy 1021 ACCCTTACTCATCCCGGGGTATGTTCATGTGTTGAACCACTCCCAACCTTGTGAGA 1080
Db 1021 ACCCTTACTCATCCCGGGGTATGTTCATGTGTTGAACCACTCCCAACCTTGTGAGA 1080
Oy 1081 GCGCTCAGCAACAGCTTCAGAAAGCCAGACAACTAGAAATATATCTCTGACATTCC 1140
Db 1081 GCGCTCAGCAACAGCTTCAGAAAGCCAGACAACTAGAAATATATCTCTGACATTCC 1140
Oy 1141 GAAGAGTTGATCATGAGATATCACAAGAGATTAACACAGCAAGTGGAGGCGCTGCTTA 1200
Db 1141 GAAGAGTTGATCATGAGATATCACAAGAGATTAACACAGCAAGTGGAGGCGCTGCTTA 1200
Oy 1201 CCACTGGAATTAACCATGATGAGAGTTGGCTGCTTCAGAGAGATCTCTTTGATTAAT 1260
Db 1201 CCACTGGAATTAACCATGATGAGAGTTGGCTGCTTCAGAGAGATCTCTTTGATTAAT 1260
Oy 1261 AACGGAGTTGGCTGGCTGGAAAGGCGCTTTTATGAGGCTGCTGCTTAAGGAGC 1320
Db 1261 AACGGAGTTGGCTGGCTGGAAAGGCGCTTTTATGAGGCTGCTGCTTAAGGAGC 1320
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Db 1261 AACGGAGTTGGCTGGCTGGAAAGGCGCTTTTATGAGGCTGCTGCTTAAGGAGC 1320
Oy 1321 ATCTATGAGGACTTGAAGATGTACAGATGGAATTAAGGCGCATGAAGGCAAGCTTTTA 1380
Db 1321 ATCTATGAGGACTTGAAGATGTACAGATGGAATTAAGGCGCATGAAGGCAAGCTTTTA 1380
Oy 1381 ATGATCCCAAGGAGCAGATCTTCTGATCCAAACATGCTGACAGCTATGATGAGCTG 1440
Db 1381 ATGATCCCAAGGAGCAGATCTTCTGATCCAAACATGCTGACAGCTATGATGAGCTG 1440
Oy 1441 TTACAGGCGCTGGAATTTTCAACAGTGTGACTGTGCGCACAGAAATCTCCCTTGAAGACCG 1500
Db 1441 TTACAGGCGCTGGAATTTTCAACAGTGTGACTGTGCGCACAGAAATCTCCCTTGAAGACCG 1500
Oy 1501 GATTTTATTAATAACTAAATCAAGCTCGCATACTTCTGATGCTTTCAGAAATTCGTGCG 1560
Db 1501 GATTTTATTAATAACTAAATCAAGCTCGCATACTTCTGATGCTTTCAGAAATTCGTGCG 1560
Oy 1561 GTGACATCAATAGATGATGTCTTGAACCTTTC 1599
Db 1561 GTGACATCAATAGATGATGTCTTGAACCTTTC 1599

RESULT 2
US-09-917-265-63/c
: Sequence 63, Application US/09917265
: Patent No. US2002052030A1
: GENERAL INFORMATION:
: APPLICANT: Wonderling, Ramani S.
: APPLICANT: Boroughs, Karen L.
: TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
: FILE REFERENCE: IM-5
: CURRENT APPLICATION NUMBER: US/09/917,265
: PRIOR FILING DATE: 2001-07-27
: PRIOR APPLICATION NUMBER: 60/223,016
: PRIOR FILING DATE: 2000-08-04
: NUMBER OF SEQ ID NOS: 109
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 63
: LENGTH: 1599
: TYPE: DNA
: ORGANISM: Canis familiaris
US-09-917-265-63

Query Match 100.0%; Score 1599; DB 10; Length 1599;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ATGACCCCTAGCAGTGTGTGATCTCTGTTTCCCTGTTTGGTGGCTGCCCTC 60
Db 1599 ATGACCCCTAGCAGTGTGTGATCTCTGTTTCCCTGTTTGGTGGCTGCCCTC 1540
Oy 61 ATGGCCATATGAGCACTGAGAAAGATGTTTATGTTTATGAGTTGAGCTGGACCTGAT 120
Db 1539 ATGGCCATATGAGCACTGAGAAAGATGTTTATGTTTATGAGTTGAGCTGGACCTGAT 1480
Oy 121 GCCCGCGAGAAATGTTGTTCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTG 180
Db 1479 GCCCGCGAGAAATGTTGTTCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTG 1420
Oy 181 ACCTCAGCAGAGCACTGAGAGTCTTAGTGTGTTGTTAAACTGTGACCATCAAGTAAA 240
Db 1419 ACCTCAGCAGAGCACTGAGAGTCTTAGTGTGTTGTTAAACTGTGACCATCAAGTAAA 1360
Oy 241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATTAAGGAGGCAAGTTTGAGCGGCTCA 300
Db 1359 GAATTTGGAGATGCTGGCCAGTATACCTGCCATTAAGGAGGCAAGTTTGAGCGGCTCA 1300
Oy 301 CTCCTGTTGATTCACAAAAAAGAGATGGAATTTGGTCCACTGATATCTTAAAGAACAG 360
Db 1299 CTCCTGTTGATTCACAAAAAAGAGATGGAATTTGGTCCACTGATATCTTAAAGAACAG 1240
Oy 361 AAAAATCCAAAAATAGATCTTTCTGAAATGTGAGGCAAAAGATTTCTTGACGTTTC 420
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Db 1239 AAGAAATCCAAAATAAGACTTTCTGAATGTGAGGCAAGAATTAATTCGTGACGTTTC 1180
QY 421 ACATGCTGCTGCTGAGGAGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTACGACA 480
Db 1179 ACATGCTGCTGCTGAGGAGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTACGACA 1120
QY 481 GGCCTTCGTGAGCCCAAGGGGTGACATCTGAGGCAAGTGCACCTTCAGCAGAGAGGCTC 540
Db 1119 GGCCTTCGTGAGCCCAAGGGGTGACATCTGAGGCAAGTGCACCTTCAGCAGAGAGGCTC 1060
QY 541 AGAGTGCACAAAGGAGATTATTAAGAGTACACAGTGCAGTGTGAGGAGGAGGCTGCTGC 600
Db 1059 AGAGTGCACAAAGGAGATTATTAAGAGTACACAGTGCAGTGTGAGGAGGAGGCTGCTGC 1000
QY 601 CCTCTGTGAGAGAGAGGCTACCCATCAGAGTGTGCTGCTGATCTATTCAGAGCTCAG 660
Db 999 CCTCTGTGAGAGAGAGGCTACCCATCAGAGTGTGCTGATCTATTCAGAGGCTCAG 940
QY 661 TATGAACACTACACAGGAGCTTCTTCATGAGACATCATCAACCCAGACCCAGACA 720
Db 939 TATGAACACTACACAGGAGCTTCTTCATGAGACATCATCAACCCAGACCCAGACA 880
QY 721 AACCTGCAGCTGAAGCATTGAAAAATTCGCGCAGCTGAGAGCTGAGCTTGGAATACCC 780
Db 879 AACCTGCAGCTGAAGCATTGAAAAATTCGCGCAGCTGAGAGCTGAGCTTGGAATACCC 820
QY 781 GACAGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
Db 819 GACAGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 760
QY 841 AAGAACTAATAGCAAAAGAAAGATACAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
Db 759 AAGAACTAATAGCAAAAGAAAGATACAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAG 700
QY 901 TGCACAGAGGATGCCAAGATCCGCGTGCAAGCCGAGACCGGCTACTATAGTTTCATCTCG 960
Db 699 TGCACAGAGGATGCCAAGATCCGCGTGCAAGCCGAGACCGGCTACTATAGTTTCATCTCG 640
QY 961 ACGGACTGCGCATCTGTGTATCAGTACAGTGTGTGCGGTGCGGCGGATGTAGAACTTGCA 1020
Db 639 ACGGACTGCGCATCTGTGTATCAGTACAGTGTGTGCGGTGCGGCGGATGTAGAACTTGCA 580
QY 1021 ACGGACTGCGCATCTGTGTATCAGTACAGTGTGTGAGGAGCTGCCAAGCTTGAGACA 1080
Db 579 ACGGACTGCGCATCTGTGTATCAGTACAGTGTGTGAGGAGCTGCCAAGCTTGAGACA 520
QY 1081 GCGGTGAGCAAGACGCTTGAGAGGCGCAGAACACTCTAGAATTTATTTCTGCACTTCG 1140
Db 519 GCGGTGAGCAAGACGCTTGAGAGGCGCAGAACACTCTAGAATTTATTTCTGCACTTCG 460
QY 1141 GAAGAACTGATCATGAACATATCACAAAGATTAACAGCAGCAGTGCAGGCGCTCTTA 1200
Db 459 GAAGAACTGATCATGAACATATCACAAAGATTAACAGCAGCAGTGCAGGCGCTCTTA 400
QY 1201 CCAGCTGAATTAACATGATGAGTGTGCTGCTGCTGAGAGAGTGTCTTGATTAAC 1260
Db 399 CCAGCTGAATTAACATGATGAGTGTGCTGCTGCTGAGAGAGTGTCTTGATTAAC 340
QY 1261 AACGGAGTTGCTGCGCTCTGAGAAAGGCTCTTTATGAGGCTGCTGCTTACAGC 1320
Db 339 AACGGAGTTGCTGCGCTCTGAGAAAGGCTCTTTATGAGGCTGCTGCTTACAGC 280
QY 1321 ATCTATGAGGAGCTTGAAGATGTACAGATGGAATTAAGGCCATGAAGCCAAAGCTTTTA 1380
Db 279 ATCTATGAGGAGCTTGAAGATGTACAGATGGAATTAAGGCCATGAAGCCAAAGCTTTTA 220
QY 1381 ATGGAATCCCAAGAGCAGATCTTTCTGATCAAAACATCTGACACTCTGCAATGAGCTG 1440
Db 219 ATGGAATCCCAAGAGCAGATCTTTCTGATCAAAACATCTGACACTCTGCAATGAGCTG 160
QY 1441 TTACAGGCTCTGATTTTCAACAGTGTGACTGTGCCAGAAATCTGCTCTGAGAGGCG 1500
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Db 159 TTACAGGCGCCGTAATTTCAACAGTGTGACTGTGCCACAGAAATCTCCCTGAGAGCGG 100
QY 1501 GATTTTATATAAACTAAATCAAGCTGTGATACCTTCTTCATGCTTTCAAGATTCGTGG 1560
Db 99 GATTTTATATAAACTAAATCAAGCTGTGATACCTTCTTCATGCTTTCAAGATTCGTGG 40
QY 1561 GTGACCATCAATGATGATGTGCTCTACTGAACTCTCC 1599
Db 39 GTGACCATCAATGATGATGTGCTCTACTGAACTCTCC 1

RESULT 3
US-09-917-265-66
: Sequence 66, Application US/09917265
: Patent No. US20020052030A1
: GENERAL INFORMATION:
: APPLICANT: Wonderling, Ramanj S.
: APPLICANT: Boroughs, Karen L.
: TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
: FILE REFERENCE: IM-5
: CURRENT APPLICATION NUMBER: US/09/917,265
: PRIOR FILING DATE: 2001-07-27
: PRIOR APPLICATION NUMBER: 60/223,016
: NUMBER OF SEQ ID NOS: 109
: SOFTWARE: Patentln version 3.1
: SEQ ID NO: 66
: LENGTH: 1533
: TYPE: DNA
: ORGANISM: Canis familiaris
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)..(1533)
: OTHER INFORMATION:
US-09-917-265-66

Query Match 95.9%; Score 1533; DB 10; Length 1533;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1533; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 ATATGGAACTGAGAAAGATGTTTATGTTGATGAGATTGAGGAGGAGGAGGAGGAGGAGG 126
Db 1 ATATGGAACTGAGAAAGATGTTTATGTTGATGAGATTGAGGAGGAGGAGGAGGAGGAGG 60
QY 127 GAGAAATGAGTGTCTCTACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGAC 186
Db 61 GAGAAATGAGTGTCTCTACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGAC 120
QY 187 GCGCAGAGCAGGAAGTCTAGTCTGTGTGTAAGTCTGACCATCCAACTGCAAGCAAAATTT 246
Db 121 GCGCAGAGCAGGAAGTCTAGTCTGTGTGTAAGTCTGACCATCCAACTGCAAGCAAAATTT 180
QY 247 GAGAGTGTGCGCAGTATACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTG 306
Db 181 GAGAGTGTGCGCAGTATACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTG 240
QY 307 TTGATTTCAAAAAAAGAGATGGAATTTGCTCAGTATCTTAAAGAACAGAAAGAA 366
Db 241 TTGATTTCAAAAAAAGAGATGGAATTTGCTCAGTATCTTAAAGAACAGAAAGAA 300
QY 367 TCCAAAAATTAAGATCTTCTGAAATGTGAGGCAAAAGATTAATTTGAGAGTTTCACATGC 426
Db 301 TCCAAAAATTAAGATCTTCTGAAATGTGAGGCAAAAGATTAATTTGAGAGTTTCACATGC 360
QY 427 TGTGCTGACGCGCAATCAGTACTGATTTGAATTCAGTGTCAAAAGTAGCAGAGGCTTC 486
Db 361 TGTGCTGACGCGCAATCAGTACTGATTTGAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420
QY 487 TCTTGACCCCCAAGGGGTGACATGTGAGCAGTGTGACACTTTTGACAGAGAGGCTGAGAGTG 546
Db 421 TCTTGACCCCCAAGGGGTGACATGTGAGCAGTGTGACACTTTTGACAGAGAGGCTGAGAGTG 480
QY 547 GACACAGGAGGATTATTAAGAGTACACAGTGTGAGTGTGAGAGAGGAGGAGGAGGAGGAG 606
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Db 481 GACACAGGATATTAAGAACTACACAGTGTGACAGAGGAGGAGTCCCTGCTCT 540
QY 607 GCCGAGGAGAGGCTACCCCTGAGGTCGGTGGATGCTATTCACAAAGTCAAGTATGAA 666
Db 541 GCCGAGGAGAGGCTACCCCTGAGGTCGGTGGATGCTATTCACAAAGTCAAGTATGAA 600
QY 667 AACTACACGAGAGGCTTCTTCATCGAGACATCATCAAAACGAGCCACCAACACG 726
Db 601 AACTACACGAGAGGCTTCTTCATCGAGACATCATCAAAACGAGCCACCAACACG 660
QY 727 CAGCTGAAGCCATTGAAAAATTTCTGGCAGCTGAGGTAGCTGGGAATACCCGACAC 786
Db 661 CAGCTGAAGCCATTGAAAAATTTCTGGCAGCTGAGGTAGCTGGGAATACCCGACAC 720
QY 787 TGGAGACCCCACTTCCCTGCTGCTGAGCATTTTGGCATACAGGCCAGGGCAAGAC 846
Db 721 TGGAGACCCCACTTCCCTGCTGCTGAGCATTTTGGCATACAGGCCAGGGCAAGAC 780
QY 847 AATAGAGAAAAGAAAGATAGACTCTGCTGAGCAAGACCTCAAGCTGCTGTCAC 906
Db 781 AATAGAGAAAAGAAAGATAGACTCTGCTGAGCAAGACCTCAAGCTGCTGTCAC 840
QY 907 AAGGATGCCAAGATCCGCTGCAAGCCGAGACCGCTACTATAGTTCACTTGGAGCCAC 966
Db 841 AAGGATGCCAAGATCCGCTGCAAGCCGAGACCGCTACTATAGTTCACTTGGAGCCAC 900
QY 967 TGGGCTCTGTGTGATGAGTGTGAGTGGGCGGAGTCTAGAAACTTGGCAACCCCT 1026
Db 901 TGGGCTCTGTGTGATGAGTGTGAGTGGGCGGAGTCTAGAAACTTGGCAACCCCT 960
QY 1027 ACTGCATCCCGGGATATGTCGAATGTTTGAACCACTCCCAACCTTGTGAGAGCCGTC 1086
Db 961 ACTGCATCCCGGGATATGTCGAATGTTTGAACCACTCCCAACCTTGTGAGAGCCGTC 1020
QY 1087 AGCAACACGCTTCAGAAAGCCAGACAACTAGAAATTTATTTCCGCACTTCCGAAG 1146
Db 1021 AGCAACACGCTTCAGAAAGCCAGACAACTAGAAATTTATTTCCGCACTTCCGAAG 1080
QY 1147 ATTGATCATGAGATATTCACAAAGATTAACACGACAGTGGAGGCTGCTTACCACTG 1206
Db 1081 ATTGATCATGAGATATTCACAAAGATTAACACGACAGTGGAGGCTGCTTACCACTG 1140
QY 1207 GAATTAACCATGATGAGAGTGGCTGCTCCAGAGACATCTCTTTGATTAACCTAACGG 1266
Db 1141 GAATTAACCATGATGAGAGTGGCTGCTCCAGAGACATCTCTTTGATTAACCTAACGG 1200
QY 1267 AGTGGCTGGGCTCTGGAAAGGCTCTTTATGAGGCTGCTGGCTTGGAGCATCTAT 1326
Db 1201 AGTGGCTGGGCTCTGGAAAGGCTCTTTATGAGGCTGCTGGCTTGGAGCATCTAT 1260
QY 1327 GAGGACTTGAAGATGTACCAAGATGAATTCAGAGGCCATGAAGCCAAAGCTTTAATGAT 1386
Db 1261 GAGGACTTGAAGATGTACCAAGATGAATTCAGAGGCCATGAAGCCAAAGCTTTAATGAT 1320
QY 1387 CCCAAGAGCAGATCTTTTGGATCAAAACATGCTGACAGCTATGATGATGCTTACAG 1446
Db 1321 CCCAAGAGCAGATCTTTTGGATCAAAACATGCTGACAGCTATGATGATGCTTACAG 1380
QY 1447 GCCGGAATTTTCAACAGTGTGAGTGGCAGAGAAATCCCTGCTGAAGCGGATTTT 1506
Db 1381 GCCGGAATTTTCAACAGTGTGAGTGGCAGAGAAATCCCTGCTGAAGCGGATTTT 1440
QY 1507 TTTAAACATTAATCAAGCTGTGATCTTTCATGCTTTTGAATTTGCTGGGAGAC 1566
Db 1441 TTTAAACATTAATCAAGCTGTGATCTTTCATGCTTTTGAATTTGCTGGGAGAC 1500
QY 1567 ATCAATAGATGATGCTACTTGTGAACCTCTCC 1599
Db 1501 ATCAATAGATGATGCTACTTGTGAACCTCTCC 1533

RESULT 4

US-09-917-265-68/c
: Sequence 68, Application US/09917265
: Patent No. US20020052030A1
: GENERAL INFORMATION:
: APPLICANT: Wonderling, Ramani S.
: APPLICANT: Borroughs, Karen L.
: TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
: FILE REFERENCE: IM-5
: CURRENT FILING DATE: 2001-07-27
: PRIOR APPLICATION NUMBER: 60/223,016
: PRIOR FILING DATE: 2000-08-04
: NUMBER OF SEQ ID NOS: 109
: SOFTWARE: Patentin version 3.1
: SEQ ID NO 68
: LENGTH: 1533
: TYPE: DNA
: ORGANISM: Canis familiaris
US-09-917-265-68
Query Match 95.9%; Score 1533; DB 10; Length 1533;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1533; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 67 ATATGGAACTGGAGAAAGATGTTATGCTTGAGAGTTGAGCTGCGACCTGATGCCCC 126
Db 1533 ATATGGAACTGGAGAAAGATGTTATGCTTGAGAGTTGAGCTGCGACCTGATGCCCC 1474
QY 127 GGAGAAATGTGTGCTCCTACCGTCCATACCCCTGAAGAAATGATCACTTGGACGTCA 186
Db 1473 GGAGAAATGTGTGCTCCTACCGTCCATACCCCTGAAGAAATGATCACTTGGACGTCA 1414
QY 187 GCGAGAGCAGTGAAGTCTTAGTTCTGTAAACCTGACCATCAAGTCAAGATTT 246
Db 1413 GCGAGAGCAGTGAAGTCTTAGTTCTGTAAACCTGACCATCAAGTCAAGATTT 1354
QY 247 GGAGATGCTGGCCATATACCTGCTCAATGAAGGAGCAAGCTTCTGAGCCGCTACTCTG 306
Db 1353 GGAGATGCTGGCCATATACCTGCTCAATGAAGGAGCAAGCTTCTGAGCCGCTACTCTG 1294
QY 307 TTGATTTCAAAAAAAGAGATGAATTTGTTCACATGATCTTAAAGAACAGAAAGAA 366
Db 1293 TTGATTTCAAAAAAAGAGATGAATTTGTTCACATGATCTTAAAGAACAGAAAGAA 1234
QY 367 TCCAAAAATTAAGATCTTCTGAAATGTGAGCAAGAAATTTATTTGACGTTTACATGC 426
Db 1233 TCCAAAAATTAAGATCTTCTGAAATGTGAGCAAGAAATTTATTTGACGTTTACATGC 1174
QY 427 TGTGGCTGAGGCGCAATCAGTACTGATTTGAAATTCATGCTCAAAAGTACAGAGGCTTC 486
Db 1173 TGTGGCTGAGGCGCAATCAGTACTGATTTGAAATTCATGCTCAAAAGTACAGAGGCTTC 1114
QY 487 TCTGACCCCAAGGGGTGACATGTGAGCAGTACCTTTCAGCAGAGAGGCTCAGAGTG 546
Db 1113 TCTGACCCCAAGGGGTGACATGTGAGCAGTACCTTTCAGCAGAGAGGCTCAGAGTG 1054
QY 547 GACAAACAGGATTTAAGAACTACACAGTGTGACAGAGGAGGAGTGCCTGCCCTCT 606
Db 1053 GACAAACAGGATTTAAGAACTACACAGTGTGACAGAGGAGGAGTGCCTGCCCTCT 994
QY 607 GCCGAGAGAGCTACCCATGAGAGTGTGTGATGCTATTCACAAAGTCAAGTATGAA 666
Db 993 GCCGAGAGAGCTACCCATGAGAGTGTGTGATGCTATTCACAAAGTCAAGTATGAA 934
QY 667 AACTACACGAGAGCTTCTTCATCGAGACATCATCAAAACGAGCCACCAACACCTG 726
Db 933 AACTACACGAGAGCTTCTTCATCGAGACATCATCAAAACGAGCCACCAACACCTG 874
QY 727 CAGCTGAAGCCATTGAAAAATTTCTGGCAGCTGAGGTAGCTGGGAATACCCGACAC 786
Db 873 CAGCTGAAGCCATTGAAAAATTTCTGGCAGCTGAGGTAGCTGGGAATACCCGACAC 814
QY 787 TGGAGACCCCACTTCCCTGCTGCTGAGCATTTTGGCATACAGGCCAGGGCAAGAC 846

[illegible]

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; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1595)
; OTHER INFORMATION:
US-09-917-265-38

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Query Match	89.48;	Score 1429.4;	DB 10;	Length 1599;
Best Local Similarity	93.48;	Pred. No. 0;		
Matches 1493;	Conservative 0;	Mismatches 106;	Indels 0;	Gaps 0;

[illegible]

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Db 901 TGCACAAAGATGCAAGATCCGGTGTCAAGCCAGAGACCGCTACTATACCTCATCTGG 960
OY 961 AGGACATGGGCATCTGTCTCATGACGTGTGGCGCGCGCGGATCTAGAAACTTCCCA 1020
Db 961 AGCAACTGGGCATCTGTCTGTAGTGTGGCGCGCGGATCTAGAAACTTCCCA 1020
OY 1021 ACCCTTACTCCATCCCGGGTATGTTCCTCAATGTTTGAACCACTCCCAACCTTGTAGA 1080
Db 1021 ACCCTTACTCCATCCCGGGGATGTTCCTCAAGTCCCTCAACCACTCCCAACCTTGTAGA 1080
OY 1081 GCCCTGACGACAGCTTTCAGAAAGCCAGACAACTCTAGAAATTAATTCCTGACCTTCC 1140
Db 1081 GCCATCAGCAACAGCTTTCAGAAAGCCAGACAACTCTAGAAATTAATTCCTGACCTTCC 1140
OY 1141 GAAGAGTTGATCATGAAAGATATCACAAAGATTAACACGACAGTGGAGGCGCTGCTTA 1200
Db 1141 GAAGAGTTGATCATGAAAGATATCACAAAGATTAACACGACAGTGGAGGCGCTGCTTA 1200
OY 1201 CCACGTGAATTAACATGATGAGATGGCTGCTCCAGAGAGATCTCTTTGATTAAT 1260
Db 1201 CCACGTGAATTAACATGATGAGATGGCTGCTCCAGAGAGATCTCTCTGATTAAT 1260
OY 1261 AACGGAGTTGCTGCTGCTGTGAAGGCTCTTTATGACGCTCTGCTGCTTACGAC 1320
Db 1261 AATGGAGTTGCTGCTGCTGTGAAGGCTCTTTATGACGACCTGCTGCTTACGAC 1320
OY 1321 ATCTATGAGGATTAAGATGATGACGATGACGATGACGATGACGATGACGATGACGAT 1380
Db 1321 ATCTATGAGGATTAAGATGATGACGATGACGATGACGATGACGATGACGATGACGAT 1380
OY 1381 ATGATGCCAAGAGGAGATCTTCTGTGATCAAAACATGCTGACGATGATGATGATGATGAT 1440
Db 1381 ATGATGCCAAGAGGAGATCTTCTGTGATCAAAACATGCTGACGATGATGATGATGATGAT 1440
OY 1441 TTACAGGCGCTGATTTCAACAGTGTGACGTGTGACGATGATGATGATGATGATGATGAT 1500
Db 1441 TTACAGGCGCTGATTTCAACAGTGTGACGTGTGACGATGATGATGATGATGATGATGAT 1500
OY 1501 GATTTTATTAACCTAAATCAACCTCTGATTAATCTTATGATGATGATGATGATGATGAT 1560
Db 1501 GATTTTATTAACCTAAATCAACCTCTGATTAATCTTATGATGATGATGATGATGATGAT 1560
OY 1561 GTGACCATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1599
Db 1561 GTGACCATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1599

ULT 6
09-917-265-40/c
: Sequence 40, Application US/09917265
: Patent No. US20020052030A1
: GENERAL INFORMATION:
: APPLICANT: Wonderling, Ramani S.
: APPLICANT: Boroughs, Karen L.
: TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
: FILE REFERENCE: IM-5
: CURRENT APPLICATION NUMBER: US/09/917,265
: CURRENT FILING DATE: 2001-07-27
: PRIOR APPLICATION NUMBER: 60/223,016
: PRIOR FILING DATE: 2000-08-04
: NUMBER OF SEQ ID NOS: 109
: SOFTWARE: Patent version 3.1
: SEQ ID NO 40
: LENGTH: 1599
: TYPE: DNA
: ORGANISM: Felis catus
: US-09-917-265-40

Query Match 89.4%; Score 1429.4; DB 10; Length 1599;
Best Local Similarity 93.4%; Pred. No. 0;
Matches 1493; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

OY 1 ATGACACCTCAGCAGTGTGTCTATCTCCGTGTTTCCCTCTTGTGCTGCCGTCCCTC 60
Db 1599 ATGATCCTCAGCAGTGTGTGTCTATCTCCGTGTTTCCCTCTTGTGCTGCCGTCCCTC 1540
OY 61 ATGGCCATATGGGAAGTGTGTTATGTTGTAGAGTTGGAGCTGGACCTGAT 120
Db 1539 ATGGCCATATGGGAAGTGTGTTATGTTGTAGAGTTGGAGCTGGACCTGAT 1480
OY 121 GCGCCCGGAGAAATGGTGTCTCAGCTGCTATACCCCTGAAGAGATGACATCAGCTGG 180
Db 1479 GCGCCCGGAGAAATGGTGTCTCAGCTGCTATACCCCTGAAGAGATGACATCAGCTGG 1420
OY 181 ACCTCAGCGAGACAGTGAAGTCTAGTTCTGTGTAATAAAGTGTGACATCAAGTCAAA 240
Db 1419 ACCTCAGCGAGACAGTGAAGTCTAGTTCTGTGTAATAAAGTGTGACATCAAGTCAAA 1360
OY 241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATTAAGAGAGCAAGTTCTGACCGCTCA 300
Db 1359 GAATTTGGAGATGCTGGCCAGTATACCTGCCATTAAGAGAGCAAGTTCTGACCGCTCA 1300
OY 301 CTCCTGTGATTCACAAAAGAGATGAAATTTGTCACGTGATATCAAGGAAAG 360
Db 1299 TTCCTCTGATTCACAAAAGAGATGAAATTTGTCACGTGATATCAAGGAAAG 1240
OY 361 AAGAAATCCAAAATTAAGATCTTTGTAATGTGAGGCAAAAGATTAATCTGACGTTTC 420
Db 1239 AAGAAATCCAAAATTAAGATCTTTGTAATGTGAGGCAAAAGATTAATCTGACGTTTC 1180
OY 421 ACATGCTGTGTGTGACGCGCAATCAGTATGATTTGAATTCAGTGTCAAAAGTACGAGA 480
Db 1179 ACCTGTGTGTGTGACGCGCAATCAGTATGATTTGAATTCAGTGTCAAAAGTACGAGA 1120
OY 481 GGCCTTGTGACCCCAAGGGGTGACATGTGTGAGCAGTGTGACGATTTGACGAGAGGGTC 540
Db 1119 GGCCTTGTGACCCCAAGGGGTGACATGTGTGAGCAGTGTGACGATTTGACGAGAGGGTC 1060
OY 541 AGAGTGACAAACAGGATTAAGAAATGACAGAGTGTGACGAGGCGCAGTCCCTGC 600
Db 1059 AGAGTGACAAACAGGATTAAGAAATGACAGAGTGTGACGAGGCGCAGTCCCTGC 1000
OY 601 CCTCTGCGGAGAGACCTTACCATGAGTGTGTGTGATGCTTATTCAGAGCTCAAG 660
Db 999 CCGGCTGCGGAGAGACCTTACCATGAGTGTGTGTGATGCTTATTCAGAGCTCAAG 940
OY 661 TATGAACATTAACACAGCAGCTTCTTCATGAGACATTCATCAACAGCAGCCACACACA 720
Db 939 TACGAAACATTAACACAGCAGCTTCTTCATGAGACATTCATCAACAGCAGCCACACAG 880
OY 721 AACCTGAGCTGAAGCCATTGAAAAATTCGCGACGCTGAGAGGTCAAGTGGAAATACCC 780
Db 879 AACCTGAGCTGAAGCCATTGAAAAATTCGCGACGCTGAGAGGTCAAGTGGAAATACCC 820
OY 781 GACACCTGAGAGACCCACATTCCTTACTTCCCTGACATTTTTCATACAGGCGCAAGGC 840
Db 819 GACACCTGAGAGACCCACATTCCTTACTTCCCTGACATTTTTCATACAGGCGCAAGGC 760
OY 841 AAGAACATGAGAAAAAGAAAGATAGACTGTGCTGAGCAAGACCTCAGCAAGTGTGTG 900
Db 759 AAGAACATGAGAAAAAGAAAGATAGACTGTGCTGAGCAAGACCTCAGCAAGTGTGTG 700
OY 901 TGCACAAAGATGCAAGATCCGCTGTGCAAGCCGAGACCGCTACTATATGATCATCTGG 960
Db 699 TGCACAAAGATGCAAGATCCGCTGTGCAAGCCGAGACCGCTACTATATGATCATCTGG 640
OY 961 AGGCACATGGGCATCTGTGTATGACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1020
Db 639 AGGCACATGGGCATCTGTGTATGACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 580
OY 1021 ACCCTTACTCCATCCCGGGTATGTTTCAATGTTTGAACCACTCCCAACCTTGTGAGA 1080
Db 579 ACCCTTACTCCATCCCGGGGATGTTTCAATGTTTGAACCACTCCCAACCTTGTGAGA 520
OY 1081 GCCGTGACGAACAGCTTTCAGAAAGGCCAGACAAACTCTAGAAATTAATTCCTGACCTTCC 1140

Db 519 GCATACACACCCCTTCAGAGCCAGACAACTTAGAATTCTTACTCTGCACCTTC 460
Qy 1141 GAAGGATTGATCATGAGCATATGCACAAAGATTAACACAGACAGTGGAGCCCTGCTTA 1200
Db 459 GAGAGATTGATCATGAGATATGCACAAAGATTAACACAGACAGTGGAGCCCTGCTTA 400
Qy 1201 CCACATGCAATTAAACGATGATGAGAGTTGCGCTTCAGAGATCTCTTTGATTA 1260
Db 399 CCACATGCAATTAAACGATGATGAGAGTTGCGCTTCAGAGATCTCTCTGTAACT 340
Qy 1261 AACGGAGTCTGCTGCTCTGAGAAAGCCCTTTTATGACGCTCTGCTTACGAC 1320
Db 339 AATGGAGCTGCTGCTCTGAGAAAGCCCTTTTATGACGCTCTGCTTACGAC 280
Qy 1321 ATCTATGAGGCTTGAACATGATGACAGATGGAATTCAGAGCCATGACGCAAGCTTTTA 1380
Db 279 ATCTATGAGGCTTGAACATGATGACAGATGGAATTCAGAGCCATGGAAGCTTTTA 220
Qy 1381 ATGATCCCAAGAGGACAGATCTTTCTGATCAAAACATGCTGACAGCTATGATGAGCTG 1440
Db 219 ATGATCTCTAAAGGCAATCTCTTCTGATCAAAACATGCTGACAGCTATGATGAGCTG 160
Qy 1441 TTACAGGCTCTGAAATTTCAAGAGTGTGACTGTGCCAGAAATCCCTTGGAAGAGCCG 1500
Db 159 TTACAGGCTCTGAAATTTCAAGAGTGTGACTGTGCCAGAAATCCCTTGGAAGAGCCG 100
Qy 1501 GATTTTAAACTTAAATGACAGCTGTGACTCTTCTTCATGCTTTTACAGATTTGCTGG 1560
Db 99 GATTTTAAACTTAAATGACAGCTGTGACTCTTCTTCATGCTTTTACAGATTTGCTGCA 40
Qy 1561 GTGACCATCAATAGATGATGCTGCTACTTGAACCTTCC 1599
Db 39 GTGACCATCAATAGATGATGATGCTGCTACTGCTTCC 1

RESULT 7
US-09-917-265-43
Sequence 43, Application US/09/917265
Patent No. US20020052030A1
GENERAL INFORMATION:
APPLICANT: Wonderlino, Kamani S.
APPLICANT: Borouhhs, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
FILE REFERENCE: IM-5
CURRENT APPLICATION NUMBER: US/09/917,265
PRIOR FILING DATE: 2001-07-27
CURRENT APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 109
SOFTWARE: PatentIn version 3.1
SEQ ID NO 43
LENGTH: 1533
TYPE: DNA
ORGANISM: Felis catus
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1533)
OTHER INFORMATION:
US-09-917-265-43

Query Match 85.9%; Score 1373; DB 10; Length 1533;
Best Local Similarity 93.5%; Pred. No. 0;
Matches 1433; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

Qy 67 ATATGCGACTGAGAAAGATGTTATGTTGAGAGTTGAGCTGCACCCCTGATGCCCCC 126
Db 1 ATATGCGAACTGAGAAAGATGTTATGTTGAGAGTTGAGCTGCACCCCTGATGCCCCC 60
Qy 127 GGAGAAATGCTGCTTACTGCTGACATACCCCTGGAAGAGATGACATGACTTGACGCTCA 186
Db 61 GGAGAAATGCTGCTTACTGCTGACATACCCCTGGAAGAGATGACATGACTTGACGCTCT 120

Qy 187 GCGAGAGCAGTAGAGTCTAGTTCGTGTAAACTCTGACCATCCAGATCAAGATTTT 246
Db 121 GACCAAGAGCAGTAGAGTCTAGGCTCTGTGTAAACTCTGACCATCCAGATCAAGATTTT 180
Qy 247 GAGATGCTGGCCAGTATACCTGCGCATAAAGAGGCAAGGTTCTGAGCCGCTACTCTG 306
Db 181 GCAGATGCTGGCCAGTATACCTGCTCATAAAGAGGCGAGGTTCTGAGCATCTGTTCCCTC 240
Qy 307 TTGATTCACAAAAAAGAGATGGATTTGGTCCACTGATATCTTTAAAGAACAGAAAGAA 366
Db 241 CTGATACACAAAAAGAGATGGATTTGGTCCACTGATATCTTTAAAGGAACAGAAAGAA 300
Qy 367 TCCAAAAAATAGATCTTTCTGAAATGTGAGGCAAGAAATATTCGGAGCTTCACATGC 426
Db 301 TCCAAAAAATAGATCTTTCTGAAATGTGAGGCAAGAAATATTCGGAGCTTTCACTGC 360
Qy 427 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 486
Db 361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420
Qy 487 TCTGACCCCAAGGGGTGACATGTGGACAGTACACTTTTCAGCAGAGAGGTGACAGT 546
Db 421 TCTGACCCCAAGAGGTGACTTGTGACAGGCACTCTCAGCAGAGAGGTGACAGT 480
Qy 547 CACACAGGATTTATTAAGAGTACACAGTGGAGTGTGAGAGGAGGAGTGCCTGCTCT 606
Db 481 GACACAGGATTTATTAAGAGTACACAGTGGAGTGTGAGAGGAGGAGTGCCTGCTCT 540
Qy 607 GCCAGAGAGGCTACCCATCGAGTCTGTGTGATGCTATTACAGAGCTCAAGTATGAA 666
Db 541 GCCAGAGAGGCTACCCATCGAGTGTGAGTGTGAGAGGCTATTACAGAGCTCAAGTATGAA 600
Qy 667 AACTACACGAGGCTTCTCATCAGAGATCATCAAAACGAGACCCACCAAAACCTG 726
Db 601 AACTACACGAGGCTTCTCATCAGAGATCATCAAAACGAGACCCACCAAAACCTG 660
Qy 727 CAGCTGAAGCCATTTGAAAAATTCCTGGCAGCGTGGAGTGTGAGTATACCCACAC 786
Db 661 CAGCTGAAGCCATTTGAAAAATTCCTGGCAGTGTGAGTGTGAGTATACCCACAC 720
Qy 787 TGGAGACCCCACTTCTCTCTCTGCTGACATTTTGCATACAGGCCCAAGGCAAGAC 846
Db 721 TGGAGACCCCACTTCTCTCTCTGCTGACATTTTGCATACAGGCCCAAGGCAAGAC 780
Qy 847 AATAGAGAAAGAAAGATAGACTGTGGTGGACAGACTCTAGCCCAAGGCTGTGGCAC 906
Db 781 AATAGAGAAAGAAAGATAGACTGTGGTGGACAGACTCTAGCCCAAGGCTGTGGCAC 840
Qy 907 AAGATGCGCAAGATTCGGGTGCAAGCCCGAGACCGCTACTATAGTTCACTCGAGGAC 966
Db 841 AAGATGCGCAAGATTCGGGTGCAAGCCCGAGACCGCTACTATAGCTCATCTGGAGCAAC 900
Qy 967 TGGCATCTGTGTCATGCAAGTGTGGCGGTGGCGGAGATCTAGAACTTGGCAACCCCT 1026
Db 901 TGGCATCTGTGTCATGCAAGTGTGGCGGTGGCGGAGATCTAGAAACTTGGCAACCCCT 960
Qy 1027 ACTCCATCCCGGGGTATCTTCCCAATGTTGAACCACTCCCAAGCTCTTGAAGACCGCTC 1086
Db 961 ACTCCATCCCGGGGTATCTTCCCAATGTTGAACCACTCCCAAGCTCTTGAAGACCGCTC 1020
Qy 1087 AGCAACAGCGTTCAGAAAGCCAGACAAACTAGATATATTCCTGCACTTCGGAAGAG 1146
Db 1021 AGCAACAGCGTTCAGAAAGCCAGACAAACTAGATATATTCCTGCACTTCGGAAGAG 1080
Qy 1147 ATTGATCATGAAGATATACAAAGAGATAAACCAAGCAGAGTGGAGGCTGCTTACCACTG 1206
Db 1081 ATTGATCATGAAGATATACAAAGAGATAAACCAAGCAGAGTGGAGGCTGCTTACCACTG 1140
Qy 1207 GAATTAACCATGAATGAGAGTGTGCTGCTGCAAGAGAGTCTGTTGATTAAGTAAAGGG 1266
Db 1141 GAATTAACCATGAATGAGAGTGTGCTGCTGCAAGAGAGTCTGTTGATTAAGTAAAGGG 1200
Qy 1267 AGTTGCCCTGGCCCTGGAAGGCGCTTTTATGACGCTCTGTGCTTAGCAGCATCTAT 1326

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Db 1201 AGTGGCCGGCCCTCAGAAAACCTTTTATGAGACCCCTGTGCTTAGCAGTATCAT 1260
1327 GAGACCTTGAGATGTACCATGGAATTTCAAGGCCATGAACCGCAACCTTTATGAT 1386
Db 1261 GAGACCTTGAGATGTACCATGGAATTTCAAGGCCATGAATGCAAAAGCTTTAATGAT 1320
1387 CCCAAGAGCGAGATCTTTCTGGATCAAAAACATGCTGACAGCTATGATGAGCTGTACAG 1446
Db 1321 CCTAAAGCGAGATCTTTCTGATCAAAAACATGCTGACAGCTATGATGAGCTGTACAG 1380
1447 GCCCTGAATTTCAACAGTGTACTGTGCGACAGAAATCCTCCCTTGAAGACCGGATTTT 1506
Db 1381 GCCCTGAATGTCAACAGTGTACTGTGCGACAGAACTCCTCTTGAAGAACCGGATTTT 1440
1507 TATAAACTAAATCAACCTGTGCTGACTTCTTCATGCTTTAGATTCGTCGGTGACG 1566
Db 1441 TATAAACTAAATCAACCTGTGCTGACTTCTTCATGCTTTAGATTCGTCGGTGACG 1500
1567 ATCAATAGATGATGCTCCTACTGAACTCTTCC 1599
1501 ATCAATAGATGATGAGCTATCTGATGCTTCC 1533

RESULT 8
US-09-917-265-45/c
: Sequence 45, Application US/09917265
: Patent No. US20020052030A1
: GENERAL INFORMATION:
: APPLICANT: Wonderling, Ramani S.
: TITLE OR INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
: FILE REFERENCE: IM-5
: CURRENT APPLICATION NUMBER: US/09/917,265
: PRIOR FILING DATE: 2001-07-27
: PRIOR APPLICATION NUMBER: 60/223,016
: PRIOR FILING DATE: 2000-08-04
: NUMBER OF SEQ ID NOS: 109
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 45
: LENGTH: 1533
: TYPE: DNA
: ORGANISM: Felis catus
US-09-917-265-45

Query Match 85.9%; Score 1373; DB 10; Length 1533;
Best Local Similarity 93.5%; Pred. No. 0;
Matches 1433; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

67 ATATGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGACCTGATGCCCC 126
Db 1533 ATATGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGACCTGATGCCCC 1474
127 GGAAATATGGTGTCTGACCTGACATACCCCTGAAGAAGTGCATCACTTTGAGACCTCA 186
Db 1473 GGAAATATGGTGTCTGACCTGACATACCCCTGAAGAAGTGCATCACTTTGAGACCTCT 1414
187 GCGCAGAGCAGTGAAGTCTAGTTCGTGTAAGTCTGACCATCAAGTCAAGAAATTT 246
Db 1413 GACCAAGACATGAAGTCTAGTTCGTGTAAGTCTGACCATCAAGTCAAGAAATTT 1354
247 GAGATGCTGGCCAGTATACCTGCCATTAAGGAGCAAGTTCTGAGCCGCTCACTCTG 306
Db 1353 GCAATATCTGGCCAGTATACCTGCCATTAAGGAGCAAGTTCTGAGCCGCTCACTCTG 1294
307 TTGATTTCAAAAAAAGAGATGAAATTTGTCGCTGATCTTAAGAGACACAGAAAGAA 366
Db 1293 CTGTATACAAAAAGAGATGAAATTTGTCGCTGATCTTAAGAGACACAGAAAGAA 1234
367 TCCAAAAATAGATCTTTCTGAATGTGAGGCAAGAAATTTCTGACGTTTACATGC 426
Db 1233 TCCAAAAATAGATCTTTCTGAATGTGAGGCAAGAAATTTCTGACGTTTACATGC 1174

427 TGTGGCTGAGCGCAATCAGTACTGATTTGAATTTCAAGTGTCAAAAGTAGCAGAGCTTC 486
Db 1173 TGTGGCTGAGCGCAATCAGTACTGATTTGAATTTCAAGTGTCAAAAGTAGCAGAGCTTC 1114
487 TCTGACCCCAAGGGGTGACATGTGGAGCACTGACCTTTAGCAGAGAGGTTCAAGTGTG 546
Db 1113 TCTGACCCCAAGGGGTGACATGTGGAGCACTGACCTTTAGCAGAGAGGTTCAAGTGTG 1054
547 GACAAAGAGGATTTTAAGAACTACACAGTGGAGTGCAGAGGGGAGTGGCTGCCCTCT 606
Db 1053 GACAAAGAGGATTTTAAGAACTACACAGTGGAGTGCAGAGGGGAGTGGCTGCCCTCT 994
607 GCCGAGGAGACCTTACCCATGAGGTGCTGTGGATGCTATTCACAAGCTCAAGTATGAA 666
Db 993 GCCGAGGAGACCTTACCCATGAGGTGCTGTGGATGCTATTCACAAGCTCAAGTATGAA 934
667 AACTACACACAGCTTCTTATCAGAGACATCATCAAAACGACGCCACCAACCAACTGTG 726
Db 933 AACTACACACAGCTTCTTATCAGAGACATCATCAAAACGACGCCACCAACCAACTGTG 874
727 CAGCTGAAGCCATTGAAAAATTTCTGGCAGCTGGAGGTCAGCTGGAAATACCCGACAC 786
Db 873 CAGCTGAAGCCATTGAAAAATTTCTGGCAGCTGGAGGTCAGCTGGAAATACCCGACAC 814
787 TGGAGCACCCCAATTCCTACTTCTCCCTGACATTTTGCATACAGGCCACGAGCAAGAAC 846
Db 813 TGGAGCACCCCAATTCCTACTTCTCCCTGACATTTTGCATACAGGCCACGAGCAAGAAC 754
847 AATAGAGAAAAAGAAAGATAGACTGTGCTGTGACAAAGACCTGACCAAGTGTGTGCAC 906
Db 753 AATAGAGAAAAAGAAAGATAGACTGTGCTGTGACAAAGACCTGACCAAGTGTGTGCAC 694
907 AAGATGCAAGATTCGCGGTGCAAGGCCGAGACCGCTACTTAACTTCACTCTGAGAGCAG 966
Db 693 AAGATGCAAGATTCGCGGTGCAAGGCCGAGACCGCTACTTAACTTCACTCTGAGAGCAG 634
967 TGGCATCTGTGTATGATGAGTGTGGCGGTGGCGGCGATCTAGAAACTTGGCAACCCCT 1026
Db 633 TGGCATCTGTGTATGATGAGTGTGGCGGTGGCGGCGATCTAGAAACTTGGCAACCCCT 574
1027 ACTGCATCCCGGGGTATGTTGCATATGTTTGAACCACTGCCAAACCTTGTTGAGAGCGGTC 1086
Db 573 ACTGCATCCCGGGGTATGTTGCATATGTTTGAACCACTGCCAAACCTTGTTGAGAGCGGTC 514
1087 AGCAACACGCTTTCAGAGAGCCGAGCAAAACCTTAGAATTTATTTCTGCTCACTTCCGAAGAG 1146
Db 513 AGCAACACGCTTTCAGAGAGCCGAGCAAAACCTTAGAATTTATTTCTGCTGCTCCGAAGAG 454
1147 ATTGATCATGAAGTATTCACAAAGATTAACACGACAGTGTGAGGCGCTGTTACCATG 1206
Db 453 ATTGATCATGAAGTATTCACAAAGATTAACACGACAGTGTGAGGCGCTGTTACCATG 394
1207 GAATTAACCATGATGAGTGTGCTGCTGCTGCTGAGAGATCTCTTGATTAACTAAGGG 1286
Db 393 GAATTAACCATGATGAGTGTGCTGCTGCTGCTGAGAGATCTCTTGATTAACTAAGGG 334
1267 AGTTGCCCTGGCTCTGGAAGGCTCTTTATGACGCGTCTGTGCTTAGCAGCATAT 1326
Db 333 AGTTGCCCTGGCTCTGGAAGGCTCTTTATGACGACCGTGTGCTTAGCAGCATAT 274
1327 GAGCACTTGAAGATGTACACAGATGGAATTCAGAGCCATGAAGCAAGCTTTTAATGAT 1386
Db 273 GAGCACTTGAAGATGTACACAGATGGAATTCAGAGCCATGAAGCAAGCTTTTAATGAT 214
1387 CCCAAGAGCGAGATCTTTCTGATCAAAACATGCTGACAGTATGATGAGCTGTTCAG 1446
Db 213 CCTAAAGGCGAGATCTTTCTGATCAAAACATGCTGACAGCTATTTAGACGTTTACAG 154
1447 GCCCTGAATTTCAACAGTGTGACTGTGCGACAGAAATCCTCTTGAAGAGCCGATTTT 1506
Db 153 GCCCTGAATGTCAACAGTGTGACTGTGCGACAGAAATCCTCTTGAAGAGCCGATTTT 94
1507 TATAAACTAAATCAAGCTCTGATATCTTCTCATGCTTTTCAGAAATTCGTGGGTGACC 1566

Db 3717 CAAACCTCTGAGGCGCCCTGACCAACGATCCCAAGCCAGACAAACTAGATTTT 3776
OY 1126 TATTCCTGACATTCGAGAGATTTGATCATGAAGATATCAAAAGGATTAACCCACACA 1185
Db 3777 TACCTTGCACCTTCTGAAAGATTTGATCATGAAGATATCAAAAGATTAACCCACACA 3836
OY 1186 GTGAGAGCCCTGCTTACCACTGGAATTAACCATGAATGAGAGATTGCCCTGCCACAGAG 1245
Db 3837 GTGAGAGCCCTGCTTACCACTGGAATTAACCATGAATGAGAGATTGCCCTGCCACAGAG 3896
OY 1246 ATCTCTTTATTAACCTAACGGAGTTGCCCTCTGGAAAGCCCTTTTATGACGGTC 1305
Db 3897 ACCCTCTTATTAACCTAACGGAGTTGCCCTCTGGAAAGCCCTTTTATGACGGTC 3956
OY 1306 CTGTGCTTACGACATCTATGAGACCTGGAAGATGATACAGATTAATTCAGGCGATG 1365
Db 3957 CTGTGCTTACGACATCTATGAGACCTGGAAGATGATACAGATTAATTCAGGCGATG 4016
OY 1366 AAGCAACGCTTTTAAATGATCCCAAGAGGAGATCTTTCTGGATCAAAACATGCTGACA 1425
Db 4017 AATGCAAACTCTGATGATGATCTTAAGAGGAGATCTTCTGATCAAAACATGCTGACA 4076
OY 1426 GCTATCGATGACCTGTTAAGGCCCCGATTTTCAACAGTGTGACTGTGCCACAGAAATCC 1485
Db 4077 GTTATTTGATGACCTGATGAGGCCCCGATTTTCAACAGTGTGACTGTGCCACAGAAATCC 4136
OY 1486 TCCCTTGAAGAGCCGATTTTATAAACTAAATCAAGCTGTGACTGTGCTTTCATGCT 1545
Db 4137 TCCCTTGAAGAGCCGATTTTATAAACTAAATCAAGCTGTGACTGTGCTTTCATGCT 4196
OY 1546 TTCAGATTCGTGCGGTGACCATCAATGATGATGCTTCTTACTGAACTTCC 1599
Db 4197 TTCAGATTCGTGCGGTGACCATCAATGATGATGCTTCTTACTGAACTTCC 4250

RESULT 10
US-09-828-825-15
; Sequence 15, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Seewoo
; APPLICANT: Kim, Han-soo
; TITLE OF INVENTION: Anti-cancer Cellular Vaccine
; FILE REFERENCE: 84906-102
; CURRENT APPLICATION NUMBER: US/09/828,825
; CURRENT FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: KR00-43498
; PRIOR FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 15
; LENGTH: 8629
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid
; NAME/KEY: misc_feature
; LOCATION: (1)..(750)
; OTHER INFORMATION: CMV enhancer and promoter
; NAME/KEY: promoter
; LOCATION: (1067)..(1085)
; OTHER INFORMATION: T7 RNA polymerase promoter
; NAME/KEY: misc_feature
; LOCATION: (1090)..(2726)
; OTHER INFORMATION: Human IL12.2 (coding sequence is 1103-2716, 10
; OTHER INFORMATION: amino acid linker at 2087-2116)
; NAME/KEY: CDS
; LOCATION: (1103)..(2716)
; OTHER INFORMATION: Human IL12.2 (10 amino acid linker)
; NAME/KEY: RBS
; LOCATION: (2752)..(3332)
; OTHER INFORMATION: IRBS sequence

NAME/KEY: misc_feature
; LOCATION: (3369)..(4263)
; OTHER INFORMATION: Human B7.1 sequence
; NAME/KEY: promoter
; LOCATION: (4383)..(4404)
; OTHER INFORMATION: T3 RNA Polymerase promoter
; NAME/KEY: polyA_signal
; LOCATION: (4414)..(4635)
; OTHER INFORMATION: SV40 Fragment containing polyadenylation signal
; NAME/KEY: rep_origin
; LOCATION: (4730)..(5185)
; OTHER INFORMATION: fl origin of replication
; NAME/KEY: misc_feature
; LOCATION: (5249)..(6616)
; OTHER INFORMATION: Neo r expression cassette
; NAME/KEY: misc_feature
; LOCATION: (7027)..(7887)
; OTHER INFORMATION: Ampicillin resistance gene
US-09-828-825-15

Query Match 77.0%; Score 1231.6; DB 10; Length 8629;
Best Local Similarity 86.2%; Pred. NO. 0;
Matches 1392; Conservative 0; Mismatches 204; Indels 18; Gaps 2;

OY 1 ATGCAACCTCAGCAGTGTGCTATCTCTGCTGCTTTCCTGCTGCTGCTCCCTC 60
Db 1103 ATGTGCTACACAGCATGCTGCTCATCTTGTTCCTGCTTTCCTGCTATCCCTCC 1162
OY 61 ATGCGCATATGCGAAGCTGAGAAAGATGTTATGTGTAGTGTGACATGCGACCTCAT 120
Db 1163 GTGGCCATATGCGAAGCTGAGAAAGATGTTATGTGTAGTGTGACATGCGACCTCAT 1222
OY 121 GCCCCCGGAAATGCTGTCTCTCACTGACCTGACCTGACCTGACCTGACCTGACCTG 180
Db 1223 GCCCTGGAAGATGCTGTCTCTCACTGACCTGACCTGACCTGACCTGACCTGACCTG 1282
OY 181 ACCTCAGCGCAGAGCAGTGAAGTCTAGTCTGTGTAATTAATCTGACATCCAGTCAAA 240
Db 1283 ACCTTGAACAGCAGTGAAGTCTAGTCTGTGTAATTAATTAATCTGACATCCAGTCAAA 1342
OY 241 GAATTTGAGATGCTGCGCAGTATACCTGCTTAAAGAGGCGACGCTTGACCGGCTCA 300
Db 1343 GAGTTTGAAGATGCTGCGCAGTATACCTGCTTAAAGAGGCGACGCTTGACCGGCTCA 1402
OY 301 CTCCTGTTGATTCACAAAAAAGAGATGAAATTTGGTCCACTGATATCTTAAGGAACAG 360
Db 1403 CTCCTGTTGATTCACAAAAAAGAGATGAAATTTGGTCCACTGATATCTTAAGGAACAG 1462
OY 361 AAAGATCCAAAAATTAAGATCTTTCTGAAATGTGAGGCAAGAAATTAATTTGACGTTTC 420
Db 1463 AAAGATCCAAAAATTAAGATCTTTCTGAAATGTGAGGCGCAAGAAATTAATTTGACGTTTC 1522
OY 421 ACATGCTGTGCTGCTGACGCAATCACTGACTGATTTGAATTAAGTCAAAAGTACAGA 480
Db 1523 ACCTGCTGTGCTGCTGACGCAATCACTGACTGATTTGAATTAAGTCAAAAGTACAGA 1582
OY 481 GCTTCTTGACCCCAAGGGGTGACATGTGAGGAGTGCACCTTTGACAGAGAGGTC 540
Db 1583 GCTTCTTGACCCCAAGGGGTGACATGTGAGGAGTGCACCTTTGACAGAGAGGTC 1642
OY 541 AGAGTGCACACAGGATTTATGAAGATACACAGTGTGCTGACAGAGGCGAGTCCCTGC 600
Db 1643 AGAGTGCACACAGGATTTATGAAGATACACAGTGTGCTGACAGAGGCGAGTCCCTGC 1699
OY 601 CCTCTGCGCGAGAGAGCTTACCCATTCAGAGTGTGAGTGTGATTCACAAAGTCAAG 660
Db 1700 CCAGCTGCTGAGGAGATGCTGCCATTTGAGGTCATGAGTGTGATTCACAAAGTCAAG 1759
OY 661 TATGAAATCTACACAGAGCTTTTTCATCAGAGACATATCAACACGAGCCACCCACA 720
Db 1760 TATGAAATCTACACAGAGCTTTTTCATCAGAGAGATATCAACACGAGCCACCCACA 1819
OY 721 AACCTGCAAGCTGAAGCCATTGAAAAATTTCTGCGACGTGAGAGTCAAGTGGGAATACCC 780


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1820 AACTTCACCTGACGACATTAAGAAATTCGCGCAGAGTGCAGCTGGGAGTACCT 1879
QY 781 GACACCTGAGACACCCCAATTCCTAGCTTCCTGACATTTTGCATACAGGCCAGGCG 840
Db 1880 GACACCTGAGAGTACATTCCTAGCTTCCTGACATTTTGCATACAGGCCAGGCG 1939
QY 841 AAGACCATATAGAGAAAGAGATAGACTCTGCTGACAGACCTGACCGACGAGCTGCG 900
Db 1940 AAGACCATATAGAGAAAGAGATAGACTCTGCTGACAGACCTGACCGACGAGCTGCG 1999
QY 901 TGGCAGAAAGATGCGAAGATCGGCTGCAAGCCGAGACCCCTACTATTAAGTTCATCTCG 960
Db 2000 TGGCAGAAAGATGCGAAGATCGGCTGCAAGCCGAGACCCCTACTATTAAGTTCATCTCG 2059
QY 961 AGCGACTGCGCATCTGTGTGATGCACTGTGTGCGCGGTGGCGGCGG-----A 1005
Db 2050 AGCGATGCGCATCTGTGTGCGCGGTGGCGGCGGTGGCGGCGGTGGCGGAGGCCCA 2119
Y 1006 TGTACAAATCTGCAACCCCTACTGCTGCGGCGGTATGCTGCATGCTTGAAGCAGCTGC 1065
Db 2120 TGGAGAAATCTGCGCGGTGCGCCTGACAGCCAGAGATGCTTGCATGCTTGAAGCAGCTGC 2179
QY 1066 CAACCTTCTTGAGAGCCGCTGAGCAACAGCTTGCAGAAAGCGCAGCAAACTGTAGAAATTA 1125
Db 2180 CAACCTTCTTGAGAGCCGCTGAGCAACAGCTTGCAGAAAGCGCAGCAAACTGTAGAAATTA 2239
QY 1126 TATTCCTGACTTCGCAAGAGATTTATCATCATGAGATATCACAAGCATTAACAGCAGCA 1185
Db 2240 TATTCCTGACTTCGCAAGAGATTTATCATCATGAGATATCACAAGCATTAACAGCAGCA 2299
QY 1186 GTGAGAGCGCTGCTTACCGATTAAGCATTAAGCATTAAGCATTAAGCATTAAGCATTAAG 1245
Db 2300 GTGAGAGCGCTGCTTACCGATTAAGCATTAAGCATTAAGCATTAAGCATTAAGCATTAAG 2359
QY 1246 ATCTCTTTGATTAACCTAACGGAGTTCCTGCGCTGCAAGCGCTCTTTATGACGCTC 1305
Db 2360 ACCTCTTTGATTAACCTAACGGAGTTCCTGCGCTGCAAGCGCTCTTTATGACGCTC 2419
QY 1306 CTGTGCTTACGACGATCTATGAGAGCTTTGAAGATGTACAGATGGAATTCAGAGCGCATG 1365
Db 2420 CTGTGCTTACGACGATCTATGAGAGCTTTGAAGATGTACAGAGTGTAGAGAGTGTAGAGCAGCATG 2479
QY 1366 AAGCGAAACCTTTTATGATGATCCCAAGAGCGAGATCTTCTGATCAAAACATGCTGCA 1425
Db 2480 AATCGAAACCTTTGATGATGATCTTCAAGAGCGAGATCTTCTGATCAAAACATGCTGCA 2539
QY 1426 GCTATGATGACGCTTACAGCGCTGCAATTTCAACACTGTGACCTGTGCGCAGAGAAATCC 1485
Db 2540 GTTATGATGACGCTTACAGCGCTGCAATTTCAACACTGTGACCTGTGCGCAGAGAAATCC 2599
QY 1486 TCCCTTTGAAGAGCGGATTTTATTAAGCTAAATCAAGCTGCTGATCTTTATGCT 1545
Db 2600 TCCCTTTGAAGAGCGGATTTTATTAAGCTAAATCAAGCTGCTGATCTTTATGCT 2659
QY 1546 TTCAGATTTGCGGCTGACCATCAATGAATGATGCTGCTTAACTGCTTCC 1599
Db 2650 TTCAGATTTGCGGCTGACCATCAATGAATGATGCTGCTTAACTGCTTCC 2713

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RESULT 11

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US-09-828-825-1
: Sequence 1, Application US/09828825
: Patent No. US20020018767A1
: GENERAL INFORMATION:
: APPLICANT: Lee, Seewoo
: APPLICANT: Kim, Han-soo
: TITLE OF INVENTION: Anti-cancer Cellular Vaccine
: FILE REFERENCE: B4906-102
: CURRENT APPLICATION NUMBER: US/09/828-825
: CURRENT FILING DATE: 2001-04-10
: PRIOR APPLICATION NUMBER: KR00-43498
: PRIOR FILING DATE: 2000-07-27

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: NUMBER OF SEQ ID NOS: 16
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO: 1
: LENGTH: 8578
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: NAME/KEY: enhancer
: LOCATION: (1)..(659)
: OTHER INFORMATION: CMV IE
: NAME/KEY: promoter
: LOCATION: (669)..(750)
: OTHER INFORMATION: CMV IE
: NAME/KEY: promoter
: LOCATION: (1067)..(1085)
: OTHER INFORMATION: T7 RNA Promoter
: NAME/KEY: mRNA
: LOCATION: (1090)..(1984)
: OTHER INFORMATION: Human B7.1 (1090-1956 is coding sequence)
: NAME/KEY: RBS
: LOCATION: (2013)..(2593)
: OTHER INFORMATION: IRES sequence
: NAME/KEY: mRNA
: LOCATION: (2627)..(4263)
: OTHER INFORMATION: Human IL12.0 (2640-4223 coding sequence, flexible
: OTHER INFORMATION: Linker at 3624-3629)
: NAME/KEY: promoter
: LOCATION: (4352)..(4431)
: OTHER INFORMATION: T3 RNA polymerase promoter
: NAME/KEY: polyA signal
: LOCATION: (4362)..(4583)
: OTHER INFORMATION: SV40 fragment containing polyadenylation signal
: NAME/KEY: rep-ori
: LOCATION: (4678)..(5133)
: OTHER INFORMATION: fl origin of replication
: NAME/KEY: misc.feature
: LOCATION: (5197)..(5564)
: OTHER INFORMATION: Neo r expression cassette
: NAME/KEY: misc.feature
: LOCATION: (6975)..(7835)
: OTHER INFORMATION: Ampicillin resistance
: OTHER INFORMATION: Description of Artificial Sequence: Plasmid
: NAME/KEY: CDS
: LOCATION: (2640)..(4223)
: OTHER INFORMATION: 1E 12.0 coding sequence - 2 amino acid linker at
: OTHER INFORMATION: 3624
: US-09-828-825-1

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Query Match 76.1%; Score 1216.6; DB 10; Length 8578;
Best Local Similarity 86.1%; Pred. No. 0;
Matches 1377; Conservative 0; Mismatches 204; Indels 18; Gaps 2;

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QY 1 ATGCACCCCTGACGACGATGTCATCTCTGTTTCCCTGCTTTCCTGCGCTCCCTC 60
Db 2640 ATGTCATCACCAGCAGTGTGTCATCTCTGTTTCCCTGCTTTCCTGCGATCCTCC 2699
QY 61 ATGCGCATATGGAGACTGAGCAAGATCTTTATGTTAGAGTTGAGCTGCGACCTGAT 120
Db 2700 GTGGCCATATGGAGACTGAGCAAGATCTTTATGTTAGAGTTGAGTTGATCCGAT 2759
QY 121 GCGCCCGGAGAAATGTTGCTGCTACCTGCGCATACCCCTGAAGAAAGATGACATCTTGG 180
Db 2760 GCGCCTTGAGAAATGTTGCTGCTACCTGCGCATACCCCTGAAGAAAGATGATCATCTGG 2819
QY 181 ACCTCAGCCGAGAGCAGTGAAGTCTAGGTTCTGTGTAACCTGACCATCAAGTCAAA 240
Db 2820 ACCTTGGACGAGAGAGTGAAGTCTAGGTTCTGTGTAACCTGACCATCAAGTCAAA 2879
QY 241 GAAATTTGAGATGCTGCGCCAGTATACCTGCGATTAAGAGAGCAAGTTTCTGACCGCTCA 300
Db 2880 GAGTTTGAAGATGCTGCGCCAGTATACCTGCGATTAAGAGAGCAAGTTTCTGAGCATTCG 2939
QY 301 CTGCTGTGATTCACCAAAAAGAGATGAATTTGGTCTCACTGATATCTTAAGGAACAG 360

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Db 2940 CTCCTGCTCTTACAAAAAGAGATGGAATTTGGTCCACGATATTTTAAAGACCG 2999
QY 361 AAGAGATCAAAAAATAGATCTTTTGAAGATGTAGCGCAAAAGTATTTCTGAGCTTTC 420
Db 3000 AAGAGAACCAAAATTAAGACTTTTGAAGATGTAGCGCGCAAAAGTATTTCTGAGCTTTC 3059
QY 421 ACATCTGCTGCTGACGGCAATCACTAGTATTTGAATTTGAAATTTGAGTCAAAAGTACAGA 480
Db 3060 ACCTCTGCTGCTGACGCACTAGTATTTGACATTTGAGTCAAAAGTCAAAAGTCAAGA 3119
QY 481 GGCCTTCTGACCCCAAGGGGTGACATGTGTAGACAGTACACTTTTCAGACAGAGGGTTC 540
Db 3120 GGCCTTCTGACCCCAAGGGGTGACAGTGTGAGCTGTACACTCTCTGCAAGAGAGTTC 3179
QY 541 AGAGTGTCAACAGGAGATTTATTAAGAGTACACAGTGTGAGTGTGACAGGGGAGTCTTC 600
Db 3180 AGAGGGGACAAACAGAGATAT---GAGTACTGAGTGTGAGTGTGACAGAGAGAGTCTTC 3236
QY 601 CCCTTGTCCGAGGAGAGCTTACCATTCGAGTGTGAGTGTGATGTATTTACAGCTCAAG 660
Db 3237 CCAGTGTGTGAGAGAGTGTGCGCATTTGAGTGTGATGTGAGTGTGCGTTCACAACTCAAG 3296
QY 661 TATGAAATACACAGAGCTTTCATTCAGACATCATCAACCAAGACCCAGCCACA 720
Db 3297 TATGAAATACACAGAGCTTTCATTCAGAGGACATCATCAACCTGACCCAGCCACA 3356
QY 721 AACCTGACGCTGAAGCATTTGAAAAATTCGCGCAGTGTGAGTGTGAGTGTGAGTATACCC 780
Db 3357 AACCTGACGCTGAAGCATTTGAAAAATTCGCGCAGTGTGAGTGTGAGTGTGAGTATACCC 3416
QY 781 GACACCTGTGAGAGCTTTCATTCCTCTGACATTTTGCATATGACAGGCCAGGGC 840
Db 3417 GACACCTGTGAGAGCTTTCATTCCTCTGACATTTTGCATATGAGTGTGAGTGTGAGG 3476
QY 841 AAGACATATAGAGAAAAAGATAGACTGTGCGACAAAGACCTCGACCCAGGTCGTG 900
Db 3477 AAGACATATAGAGAAAAAGATAGACTGTGCGACAAAGACCTCGACCCAGGTCGTG 3536
QY 901 TGCCACAAGATGCCAAGATCCGCGTGTGCAAGCCGACGAGACCGTACTATATGTTACTCTG 960
Db 3537 TGCCGCAAAATATGCCAGATTAGCTGTGCGGCGCAGAGACCGTACTATATGTTACTCTG 3596
QY 961 AGGCATGTGGCATCTGTGTCTCATGCACTGTGCGGTGGCGCGGATCTAGAAACTTGGCA 1020
Db 3597 AGGCATGTGGCATCTGTGTCTCTGCACT-----CCATGTGAGAAACCTCTCC 3641
QY 1021 ACCCTTACTCATCCCGGATATGTTCCATGTGTGAACCACTCCCAACCTGTTGAGA 1080
Db 3642 GTGGCACTCCAGACCGAGATGTTCCTTCCACTCCCAAACTGCTGTAGG 3701
QY 1081 GCGGTACAGCAACGCTGTGCAAGGCGACAACTCTAGAAATTTATTTCTGCACTTC 1140
Db 3702 GCGGTACAGCAACGCTGTGCAAGGCGCGACAACTCTAGAAATTTATTTCTGCACTTC 3761
QY 1141 GAAGGATTTGATCATGAGATATCAAAAGATTAACCAGACGAGTGTGAGGCTGTGTA 1200
Db 3762 GAAGGATTTGATCATGAGATATCAAAAGATTAACCAGACGAGTGTGAGGCTGTGTA 3821
QY 1201 CCACGTGAATTAACCATGATGAGAGTGTGCTGCTTCAGAGAGATCTCTTTGTAAT 1260
Db 3822 CCATTTGGAATTAACCAAGATGAGAGTGTGCTTAAATTTCCAGAGAGACTCTTTCTTAAT 3881
QY 1261 AAGGGAGTTCCTGTGCTGTGGAAGGCTCTTTTATGAGCGTCTGTGCTTATGAGCG 1320
Db 3882 AATGTAGAGTTCCTGTGCTGTGGAAGGCTCTTTTATGAGCGTCTGTGCTTATGAGCG 3941
QY 1321 ATCTATGAGCTTGAATGATTAACAGATGAGATTCAGAGGCGCATGAGCAAGCTTTTA 1380
Db 3942 ATTATGAGAGCTTGAATGATTAACAGATGAGATTCAGAGGCGCATGAGCAAGCTTTTG 4001
QY 1381 ATGATCCCAAGAGAGATTTCTGTGATCAAAACATGCTGACAGCTATGATGAGCTG 1440

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Db 4002 ATGATCCCTAAGAGGACAGATCTTCTAGATCAAAACATGCTGCGAGTTATGATGAGCTG 4061
QY 1441 TTACAGCCCTGGAATTTTACAGAGTGTGACTGTGCGACAGAAATCTCTGCTTGAAGCGG 1500
Db 4062 ATGCAAGGCCCTGAATTTTCAACAGTGAAGTGTGCGACAGAAATCTCTGCTTGAAGCGG 4121
QY 1501 GATTTTATTAACCTAATAATCAAGCTGTGACATCTTCTTCAATGCTTTTGAAGATTCGCG 1560
Db 4122 GATTTTATTAACCTAATAATCAAGCTGTGACATCTTCTTCAATGCTTTTGAAGATTCGCG 4181
QY 1561 GTGACCATCAATAGATGATGCTTCTACTTGAAGCTTTC 1599
Db 4182 GTGACCATCAATAGATGATGCTTCTACTTGAAGCTTTC 4220

RESULT 12
US-09-828-825-3
: Sequence 3, Application US/09828825
: Patent No. US20020018767A1
: GENERAL INFORMATION:
: APPLICANT: Kim, Han-soo
: TITLE OF INVENTION: Anti-cancer Cellular Vaccine
: FILE REFERENCE: 84906-102
: CURRENT APPLICATION NUMBER: US/09/828,825
: PRIOR FILING DATE: 2001-04-10
: PRIOR APPLICATION NUMBER: KR00-43498
: NUMBER OF SEQ. ID NOS: 16
: SOFTWARE: patentin Ver. 2.1
: SEQ. ID NO 3
: LENGTH: 8578
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: plasmid
: NAME/KEY: enhancer
: LOCATION: (1)..(659)
: OTHER INFORMATION: CMV IE Enhancer
: NAME/KEY: promoter
: LOCATION: (669)..(750)
: OTHER INFORMATION: CMV IE Promoter
: NAME/KEY: misc_feature
: LOCATION: (890)..(1002)
: OTHER INFORMATION: Intervening Sequence
: NAME/KEY: promoter
: LOCATION: (1067)..(1085)
: OTHER INFORMATION: T7 RNA polymerase promoter
: NAME/KEY: misc_feature
: LOCATION: (1090)..(1984)
: OTHER INFORMATION: Human B7.1 (1090-1956 is coding sequence)
: NAME/KEY: RBS
: LOCATION: (2013)..(2593)
: OTHER INFORMATION: IRES sequence
: NAME/KEY: misc_feature
: LOCATION: (2627)..(4263)
: OTHER INFORMATION: Human IL12.0 sequence (2640-4217 is coding
: NAME/KEY: promoter
: LOCATION: (4346)..(4425)
: OTHER INFORMATION: T3 RNA polymerase promoter
: NAME/KEY: polyA_signal
: LOCATION: (4356)..(4577)
: OTHER INFORMATION: SV40 fragment containing polyadenylation signal
: NAME/KEY: rep_origin
: LOCATION: (4672)..(5127)
: OTHER INFORMATION: fl origin of replication
: NAME/KEY: misc_feature
: LOCATION: (5191)..(6558)
: OTHER INFORMATION: Neo r expression cassette
: NAME/KEY: misc_feature
: LOCATION: (6969)..(7829)
: OTHER INFORMATION: Ampicillin resistance

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NAME/KEY: CDS
 LOCATION: (2640)..(4217)
 OTHER INFORMATION: IL12.0 coding sequence - no linker
 US-09-828-825-3

Query Match 76.1% Score 1216.6 DB 10; Length 8578;
 Best Local Similarity 86.1% Pred. No. 0;
 Matches 1377; Conservative 0; Mismatches 204; Indels 18; Gaps 2;

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QY 1 ATGCACCCCTGACGAGTTGGTCATCTCTGGTTTCCCTGCTTGGCTGCGTCCCTC 60
   ||| | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2640 ATGTGTACACGACGCTTGTCATCTCTGGTTTCCCTGCTTGGCTGCGTCCCTC 2659
QY 61 ATGGCCATATGGGAACTGGAGAAAGATGTTATGTTGAGTGGAGTGGACCCCTGAT 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2700 GTGGGCATATGGAACTGAAAGAAAGATGTTATGTTGAGTGGAGTGGATCGGAT 2759
QY 121 GCGCCGGAGAAATGGTGGTCTGACCTGCGCATACCCCTGAAAGAGATGACATCACTTGG 180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2760 GCGCCGGAGAAATGGTGGTCTGACCTGCGCATACCCCTGAAAGAGATGATGATCACTTGG 2819
QY 181 ACCTGACCCGACAGCAGTGAAGTCTAGCTTCTGGTAAACTGTGACATCCAGTCAAA 240
   ||| | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2820 ACCTTGACCCGACAGCAGTGAAGTCTAGCTTCTGGTAAACTGTGACATCCAGTCAAA 2879
QY 241 GAATTTGAGATGCTGCGCAGTATACCTGCGCATAAAGAGCGAAGTTCGAGCGCTCA 300
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2880 GAATTTGAGATGCTGCGCAGTATACCTGCGCATAAAGAGCGAAGTTCGAGCGCTCA 2939
QY 301 CTCCTGTTGATTCACAAAAAAGAGATGGAATTTGGTGCACATGATATCTTAAAGAACAG 360
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2940 CTCCTGTTGATTCACAAAAAAGAGATGGAATTTGGTGCACATGATATCTTAAAGAACAG 2999
QY 361 AAGAAATCCAAAAATAGATTTCTTGAATGTGAGGCAAAAGATTTATCTGACGCTTTC 420
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3000 AAGAAATCCAAAAATAGATTTCTTGAATGTGAGGCAAAAGATTTATCTGACGCTTTC 3059
QY 421 ACATGTGCTGCTGACGCAATCACTGATGATTTGAAATTCAGTTCAAAATAGTACCA 480
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3060 ACCTGTGCTGCTGACGCAATCACTGATGATTTGAAATTCAGTTCAAAATAGTACCA 3119
QY 481 GCGCTTCTGTACCCCAAGGGGTGACATGTGGAGCAGTGAACCTTTCACACAGAGAGGTC 540
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3120 GCGCTTCTGTACCCCAAGGGGTGACATGTGGAGCAGTGAACCTTTCACACAGAGAGTC 3179
QY 541 AGAGTGGCAACAGGATTTATAAGAAAGTACAGAGTGAAGTGTGAGAGGGCGAGTCTGC 600
   ||| | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3180 AGAGTGGCAACAGGATTTATAAGAAAGTACAGAGTGAAGTGTGAGAGGGCGAGTCTGC 3236
QY 601 CCTGTGCGGAGAGAGCTTACGCAATCGAGGTGCTGATGCTATTCACAAAGCTCAAG 660
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3237 CGAGCTGCGAGAGAGTGTCCCATTTGAGTCAATGATGATGCTTTCACAAAGCTCAAG 3296
QY 661 TATGAAACTAGACAGCAGCTTCTTCATCAGAGACATCATCAAAACAGACCCACACCA 720
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3297 TATGAAACTAGACAGCAGCTTCTTCATCAGAGACATCATCAAAACAGACCCACACCA 3356
QY 721 AACCTGGACCTAGAGCATTGAAAAATTCGCGGACGTGAGAGTGAAGTGAATACCCC 780
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3357 AACCTGGACCTAGAGCATTGAAAAATTCGCGGACGTGAGAGTGAAGTGAATACCCC 3416
QY 781 GACACCTGAGCAGCAGCATTTCTACTCTCTGCTGACATTTTGGCATACAGGCCAGGGC 840
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3417 GACACCTGAGCAGCAGCATTTCTACTCTCTGCTGACATTTTGGCATACAGGCCAGGGC 3476
QY 841 AAGAAACATAGAGAAAGAAAGATAGACTGTGCGTGACAGAGACCTCAAGCAAGTCTGTG 900
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3477 AAGAAACATAGAGAAAGAAAGATAGACTGTGCGTGACAGAGACCTCAAGCAAGTCTGTG 3536
QY 901 TGGCAAAACGATGGCAAGTTCGCGGTGCAAGCCGAGACCGGTACTATAGTTCACTCTGG 960
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3537 TGGCCCAAAATGCCAGGATTAAGCTGGGGGCCAGAGCCGCTACTATAGCTCACTCTGG 3596

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QY 961 AGGACTGGGCACTGTGTCATGACAGTGTGGCGGGGCGGATCTAGAAACTTGCCA 1020
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Db 3597 AGGCAATGGGCATCTGTGCGCTGCAGT -----CATGGGAAACCTGCCCC 3641
QY 1021 ACCCTTACTCCATCCCGGGGATGTTGCCAATGTTTGAACCACTCCCAAACTTTGTGAGA 1080
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3642 GTGGCCACTCCAGAGCCAGAGAAATGTTCCATGCTTCACACTCCCAAAACCTGCGAGG 3701
QY 1081 GCGGTGACACACGCTTGAGAAAGCCACAGAAACTCTAGAAATATATCTGACACTTCC 1140
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3702 GCGGTGACACACGCTTGAGAAAGCCACAGAAACTCTAGAAATATATCTGACACTTCC 3761
QY 1141 GAAAGATTTGATCATCAATATATCAAAAGATATAAACAGACAGAGTGGAGGCCCTGTTA 1200
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3762 GAAGAGATTTGATCATCAATATATCAAAAGATATAAACAGACAGAGTGGAGGCCCTGTTA 3821
QY 1201 CCATGGGAATTTAACATGATAGAGATGTTGCCGTGCTCAGAGAGATCTCTTGAATAACT 1260
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3822 CCATTTGGAATTTAACAGAGATGAGAGTGTGCTTAATTCAGAGAGACCTCTTTCATAACT 3881
QY 1261 AACGGAGTTGCTGCGCTCTGTGAAAGGCCCTCTTTTATGAGGTCCTGTGCTTAAAGCAGC 1320
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Db 3882 AATGGAGTTGCTGCGCTCTGTGAAAGGCCCTCTTTTATGAGTGTGCTTAAAGCAGC 3941
QY 1321 ATCTATGAGGACTTGAAGATGTACCAAGATGGAATTCAGCGCATGACCCAAAGCTTTTA 1380
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3942 ATTTATGAGGACTTGAAGATGTACCAAGATGGAATTCAGCGCATGAAATCAAGCTTTG 4001
QY 1381 ATGATCCCAAGAGGAGATCTTCTGTGATCAAAACATGCTACAGCTATCATGATAGCTG 1440
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4002 ATGATCTCAAGAGGAGATCTTCTGTGATCAAAACATGCTGACAGTATATGATAGCTG 4061
QY 1441 TTACAGCGCCCTAATTTCAACAGTGTGACTGTGCCACAGAAATCTCCCTTGAAGACCG 1500
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4062 ATGACAGGCCCTAATTTCAACAGTGTGACTGTGCCACAAAAATCTCCCTTGAAGACCG 4121
QY 1501 GATTTTATAAAGCTAAATCAAGCTGTGACTGTTCAAGCTTTCAGAAATTCAGAAATTCG 1560
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4122 GATTTTATAAAGCTAAATCAAGCTGTGACTGTTCAAGCTTTCAGAAATTCAGAAATTCG 1619
QY 1561 GTGACCATCAATGATGATGATGCTTCTACTTGAATCTTCC 1599
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Db 4182 GTGACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4181

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RESULT 13
 US-09-828-825-5
 : Sequence 5, Application US/09828825
 : Patent No. US20020018767A1
 : GENERAL INFORMATION:
 : APPLICANT: Lee, Han-soo
 : TITLE OF INVENTION: Anti-cancer Cellular Vaccine
 : FILE REFERENCE: 84906-102
 : CURRENT APPLICATION NUMBER: US/09/828,825
 : PRIOR APPLICATION NUMBER: 2001-04-10
 : PRIOR FILING DATE: 2000-07-27
 : NUMBER OF SEQ ID NOS: 16
 : SOFTWARE: PatentIn Ver. 2.1
 : SEQ ID NO 5
 : LENGTH: 8623
 : TYPE: DNA
 : ORGANISM: Artificial Sequence
 : FEATURE:
 : NAME/KEY: misc_feature
 : LOCATION: (1)..(750)
 : OTHER INFORMATION: CMV enhancer and promoter
 : NAME/KEY: misc_feature
 : LOCATION: (890)..(1002)
 : OTHER INFORMATION: Intervening sequence
 : NAME/KEY: promoter
 : LOCATION: (1067)..(1085)

OTHER INFORMATION: T7 RNA polymerase promoter
NAME/KEY: misc_feature
LOCATION: (1090)..(1984)
OTHER INFORMATION: Human B7.1 (1090-1956 is coding sequence)
NAME/KEY: RBS
LOCATION: (2013)..(2593)
OTHER INFORMATION: IRES sequence
NAME/KEY: misc_feature
LOCATION: (2627)..(4278)
OTHER INFORMATION: Human IL12.3 - 2640-4268 is coding sequence,
OTHER INFORMATION: flexible linker from 3606-3650
NAME/KEY: CDS
LOCATION: (2640)..(4268)
OTHER INFORMATION: IL 12.3 coding sequence - has 28 amino acid linker
OTHER INFORMATION: sequence
NAME/KEY: promoter
LOCATION: (4398)..(4407)
OTHER INFORMATION: T3 RNA polymerase promoter
NAME/KEY: polyA_signal
LOCATION: (4408)..(4629)
OTHER INFORMATION: SV40 fragment containing polyadenylation signal
NAME/KEY: rep_origin
LOCATION: (4724)..(5179)
OTHER INFORMATION: fl origin of replication
NAME/KEY: misc_feature
LOCATION: (5243)..(6610)
OTHER INFORMATION: Neo r expression cassette
NAME/KEY: misc_feature
LOCATION: (7021)..(7881)
OTHER INFORMATION: Ampicillin resistance
OTHER INFORMATION: Description of Artificial Sequence: plasmid
us-09-828-825-5

Query Match 76.1%; Score 1216.6; DB 10; Length 8623;
Best Local Similarity 85.5%; Pred. No. 0;

Matches 1392; Conservative 0; Mismatches 204; Indels 33; Gaps 2;

QY 1 ATGCACCTCAGACAGTGGTCACTCCGTTTCCCGTTTGGCTGGCGCTCCCTC 60
DB 2640 ATGCTCACCAGCAGATGGTCACTCTGTTTCCCGTTTGGCTGGCGCTCCCTC 2699
QY 61 ATGGCCATATGGGAAGTGGGAAGATGGTTATGTTAGAGTTGGACTGGCAACCTCAT 120
DB 2700 GTGGCCATATGGGAAGTGGGAAGATGGTTATGTTAGAGTTGGACTGGCGGAT 2759
QY 121 GCCCCGAGGAATGGTGGTCTCCTCCTCCATCCATACCCCTGAAGAAGATGACATCTGG 180
DB 2760 GCCCCTGAGGAATGGTGGTCTCCTCCTCCTGACACCCCTGAAGAAGATGATACCTGG 2819
QY 181 ACCTCAGCCGACAGAGTGAAGTCTAGTTCCTGTTAAACTCTGACCATCCAGTCAAA 240
DB 2820 ACCTTGGACCGAGAGAGTGAAGTCTAGTTCCTGTTAAACTCTGACCATCCAGTCAAA 2879
QY 241 GAATTTGAGAGTGGTGGCAGATACCTGCCATTAAGAGAGGCAAGTTCTGACCGCA 300
DB 2880 GAGTTTGAAGATGCTGGCGCAGTACACCTGTGACAAAGAGGAGGAGCTTCAAGCATTCG 2939
QY 301 CTCCTGTTGATTCACAAAAGAGAGATGAATTTGGTCCATGATATCTTAAAGACAG 360
DB 2940 CTCCTGCTGCTTCAACAAAAGAGAGATGAATTTGGTCCATGATATCTTAAAGACAG 2999
QY 361 AAGAGATCCAAAATAGATCTTCTTGAATGTGAGGCAAAAGATTAATCTGAGCGTTTC 420
DB 3000 AAGAGATCCAAAATAGATCTTCTTGAATGTGAGGCAAAAGATTAATCTGAGCGTTTC 3059
QY 421 ACATGCTGGTGGCTGAGGCAATCAGTACTGATTTGAATTCAGTGTCAAAAGTACGCA 480
DB 3060 ACCTGGTGGTGGCTGAGGCAATCAGTACTGATTTGAATTCAGTGTCAAAAGTACGCA 3119
QY 481 GGCCTTCTGACCCGCAAGGGGTGATGATGGAGCAGTCACTTTGACGAGAGGGGTC 540
DB 3120 GGCCTTCTGACCCGCAAGGGGTGATGATGGAGCAGTCACTTTGACGAGAGAGGTC 3179

QY 541 AGAGTGACAAACAGGATTTAAGAGTACACAGTGAAGTGTCAAGAGGAGTGGCTGC 600
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DB 3237 CGAGCTGTGAGGAGAGTCTCCCATTTGAGGTCAATGGTGGTGGCTTCAACACCTCAAG 3296
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DB 3297 TATGAACCTACACGAGGCTTCTTCATGAGAGCATCATCAAAACGAGCCAGCCGCA 3356
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DB 3597 AGCGAATGGCATCTGTGTATGACAGTGGTGGCGGTGGCGGGCG----- 1004
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QY 1231 CTGGCTTCCAGAGAGATCTTTGATTAACGAGGAGTGGCTGGCTGGAAGGCC 1290
DB 3897 CTAAATTTCCAGAGAGATCTTTGATTAACGAGGAGTGGCTGGCTGGAAGGCC 3956
QY 1291 TCTTTTATGAGGCTCTGTGCTTATGACAGCTATGAGGAGCTTGAAGATATACACATG 1350
DB 3957 TCTTTTATGAGGCTCTGTGCTTATGAGGAGCTTATGAGGAGCTTGAAGATATACACATG 4016
QY 1351 GAATTCAGGCCATGAAGCAAAAGCTTTTAATGATCCCAAGAGCAGATCTTTCTGAT 1410
DB 4017 GAGTTCAAGACCATGAATGCAAAAGCTTCTGATGATCTTGAAGAGCAGATCTTTCTGAT 4076
QY 1411 CAANAACATGCTGACAGCTATGATGAGCTGTTACAGGCGCTGAATTTCAACAGTGTGACT 1470
DB 4077 CAANAACATGCTGACAGCTATGATGAGCTGTTACAGGCGCTGAATTTCAACAGTGTGACT 4136
QY 1471 GTGCCACAGAAATCTCTCTTGAAGAGCGGATTTTATATAAATCAAAATCAACTCTGC 1530
DB 4137 GTGCCACAGAAATCTCTCTTGAAGAGCGGATTTTATATAAATCAAAATCAACTCTGC 4196
QY 1531 ATACTTCTTCAATGCTTTTCAGATTCGCGGTGACCAATCAATGAATATGCTTACTACTG 1590
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QY 1591 AACTCTTCTGC 1599

|||||
Db 2300 GATAAACCACACAGTGGAGCCGTTTACCAATTGAATTACCAAGAAAGAGATTGC 2359
QY 1231 CTGGCTCCACAGAGATCTTTGTATTAACGAGGAGTTCGCTGGCCCTCGAAAGGCG 1290
Db 2360 CTAATTCACAGAGACCTCTTTCATTAAGTATGAGGAGTCCCTGGCCCTCCAGAAAGCC 2419
QY 1291 TCTTTATGAGCGTCTGTGCTTACGAGCATATGAGAGCTTGAAGATGTACAGATG 1350
Db 2420 TCTTTATGAGCGCTGTGCTTACGAGCATATGAGAGCTTGAAGATGTACAGATG 2479
QY 1351 GAATTCAGGCGATGACGCAAGCTTTTATGATGCCAAGAGGCGAGATCTTCTGAT 1410
Db 2480 GAGTTCAGGCGATGACGCAAGCTTTTATGATGCCAAGAGGCGAGATCTTCTGAT 2539
QY 1411 CAATACATGCTGACGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1470
Db 2540 CAATACATGCTGACGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2599
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QY 1531 ATACTTCTCATGCTTTCAGAAATTCGTGCGGTGACCATCATAGATGATGCTACTTG 1590
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Db 2720 AATGCTTTC 2728
RESULT 15
US-09-828-825-9
: Sequence 9, Application US/09828825
: Patent No. US20020018767A1
: GENERAL INFORMATION:
: APPLICANT: Lee, Seewoo
: APPLICANT: Kim, Han-soo
: TITLE OF INVENTION: Anti-cancer Cellular Vaccine
: FILE REFERENCE: 84906-102
: CURRENT APPLICATION NUMBER: US/09/828,825
: PRIOR APPLICATION NUMBER: KR00-43498
: PRIOR FILING DATE: 2000-07-27
: NUMBER OF SEQ ID NOS: 16
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 9
: LENGTH: 8638
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: plasmid
: NAME/KEY: misc.feature
: LOCATION: (1)..(750)
: OTHER INFORMATION: CMV enhancer and promoter
: NAME/KEY: misc.feature
: LOCATION: (890)..(1002)
: OTHER INFORMATION: Intervening sequence
: NAME/KEY: promoter
: LOCATION: (1067)..(1085)
: OTHER INFORMATION: T7 RNA polymerase promoter
: NAME/KEY: misc.feature
: LOCATION: (1090)..(1984)
: OTHER INFORMATION: Human B7.1 (1090-1954 is coding sequence)
: NAME/KEY: RBS
: LOCATION: (2013)..(2593)
: OTHER INFORMATION: IRES sequence
: NAME/KEY: misc.feature
: LOCATION: (2627)..(4293)
: OTHER INFORMATION: Human IL12.4 (coding sequence is 2640-4283, 33
: NAME/KEY: CDS
: OTHER INFORMATION: amino acid linker at 3606-3706)

: LOCATION: (2640)..(4283)
: OTHER INFORMATION: IL12.4 coding sequence (33 amino acid linker)
: NAME/KEY: promoter
: LOCATION: (4392)..(4413)
: OTHER INFORMATION: T3 RNA polymerase promoter
: NAME/KEY: polyA_signal
: LOCATION: (4423)..(4644)
: OTHER INFORMATION: SV40 fragment containing polyadenylation signal
: NAME/KEY: rep.origin
: LOCATION: (4739)..(5194)
: OTHER INFORMATION: El origin of replication
: NAME/KEY: misc.feature
: LOCATION: (5258)..(6625)
: OTHER INFORMATION: Neo r expression cassette
: NAME/KEY: misc.feature
: LOCATION: (7036)..(7896)
: OTHER INFORMATION: Ampicillin resistance
US-09-828-825-9
Query Match 75.1%; Score 1201.6; DB 10; Length 8638;
Best local similarity 84.7%; Pred. No. 0;
Matches 1392; Conservative 0; Mismatches 204; Indels 48; Gaps 2;
QY 1 ATGCAACCTCAGCAGTTGTCATCTCCTGCTTTCCCTGTTTGTGCGCTCCCTC 60
Db 2640 ATGCTGACACGACGAGTGTGCTATCTTGTTCCTGCTTTTCTGCGATCTCCCTC 2699
QY 61 ATGGCCATATGGAAGTGGAGAAAGATGTTTATGTTGATGAGAGTGGACGACCTGAT 120
Db 2700 GTGGCCATATGGAAGTGGAGAAAGATGTTTATGTTGATGAGAGTGGATTCGGAT 2759
QY 121 GCCCCGAGAAATGTGTCTCCTACCTGCCATACCCCTGAAGAAGATGACATCTTG 180
Db 2760 GCCCTGAGAAATGTGTGCTCCTACCTGCCATACCCCTGAAGAAGATGATGATCCTG 2819
QY 181 ACCTCAGCGCAGACAGTGAAGTCTTAGTCTGTGTAAACTGTGACCATTCGAAGTAAA 240
Db 2820 ACCTTGAACGACGACGATGAGTGTAGGCTGTGCAAAACCCCTGACCATTCGAAGTAAA 2879
QY 241 GAATTTGAGATGCTGTGCGCAGTATACCTGATTAAGGAGGCAAGTTCGAGCGCTTC 300
Db 2880 GAGTTTGAAGATGCTGTGCGCAGTATACCTGATTAAGGAGGCAAGTTCGAGCGCTTC 2939
QY 301 CTCCTGTTGATTCACAAAAGAAAGATGAATTTGTCACATGATCTTAAGGAACAG 360
Db 2940 CTCCTGCTGCTTCAAAAAGAAAGATGAATTTGTCACATGATCTTAAGGAACAG 2999
QY 361 AAGCAATCCAAAATTAAGATCTTCTGAATGTGAGGCAAAAGATTTATTCGAGCGTTTC 420
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QY 421 ACATGCTGTGCTGTGAGCGCATGATGATGATTTGAATTCAGTGTCAAAAGAGCAGA 480
Db 3060 ACATGCTGTGCTGTGAGCGCATGATGATGATTTGAATTCAGTGTCAAAAGAGCAGA 3119
QY 481 GCGTTTCTGACCCCAAGGGGTGACATGTGAGCAGTGAACATTTGACGAGAGGGTC 540
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Db 3237 CCAGCTGCTGAGAGAGTGTGCCATTTGAGGTGATGATGATGATGATGATGATGATGAT 3296
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Db 3417 GACAGCTGGAGTACTCCACTTCTCTACTTCTCCTGACATTCTGGCTTCAGGTCGAGGC 3476
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Search completed: January 15, 2003, 16:51:27
Job time : 120 secs

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Craniata; Rodentia; Sciurognathi; Muridae; Mus.

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[illegible]

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): Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTNN-3'',
size-selected for average insert size 2.5 kb and
normalized to RCF 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIH/NICRI, National
Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT      188 a      245 c      226 g      149 t
ORIGIN
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Best Local Similarity 81.5%   Prid: No. 6,1e+48;
Matches 273;   Conservative 0;   Mismatch 59;   Indels 3;   Gaps 2;

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QY	1067	AAACCTTGTGAGAGCCGTCAGCAACACGCTTCAGAGAGGCCAGACAACTAGAAATTAT	1126
QY	1067		
Db	541	AAACCTTCCTTGAGGGCCCTGCACAAACATGTCTCCAGACAGGCCAGACAACTAGAAATTAT	600
QY	1127	ATTCTCTGACTTTCGAGAGAGATTGATCTCTGAAGATATATCAAAAGATATAAACCAAGACAG	1186
QY	1127		
Db	601	ACCTTGTGACTTTCGAGAGAGATGCATCATGAGAGATATATCAAAACATATAAACCAAGACAG	660
QY	1187	TGAGAGGCTCTTTCACCATCGAATTAACCATGAATGAGAGATGCTCTGCCTCCACAGAGA	1246
QY	1187		
Db	661	TGAGAGGCTCTTTCACCATCGAATTAACCAAGAGATGAGAGTTGC--TAATATCCAGAGAGAGA	718
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[illegible]

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/clone="IMAGE:5240216"
/clone_1ib="NIH_MGC_121"
/lab_host="DH10B"
/note="Organ: brain; Vector: PCMV-SPORT6; Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
fetal brains, female age 20 weeks, female age 24 weeks,
and male age 26 weeks. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
0.7-3.5 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Grubert
(Invitrogen). Research Genetics tracking code 017. Note:
this is a NIH_MGC Library."

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Query Match	12.6%	Score 202.2	DB 13	Length 1099
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Db 741	GGCCCTGTGCTTTASTACTATTTATGAAGAC-TGAAGATGTACAGGTGGATTCACAGC	683		
QY 1362	CATGACCGCAAGACTT-TTAATGCATGCCAAGAGGAGACATCTTTCTGATCAAAACATGC	1420		
Db 682	CATGAATGCAAGAGCTTCTCTGATGCATGATCTCTAAGAGGACATCTTCTPAATCAAAACATGC	623		
QY 1421	TGACAGATGATGATGAGTGTGTACAGGCCGCAATTTCAACAGTGTGACTGTGCCACAGA	1480		
Db 622	TGCGAGTATTATGATGAGTGTGATGCAGGCCGCAATTTCAACAGTGTGACTGTGCCACANA	563		
QY 1481	AATCTTCGCTTGAAGAGCGGAT--TTTATATAAACTAAATCAAGCTCTGCATCTCT	1538		

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Db	562	ATATCCCTTGAACACGAGATGTTATTAACAACTGAATCAAGCTCTGATCTTCT	503						
Oy	1539	TCATCCTTTGACAAATTCGTCGCGTCACCATCATATGAAATGATGTCCTACTTAACTCTTC	1598						
Db	502	TCATCCTTTGACAAATTCGCGGAGTACATTCATGATAGAGTGAAGTACATCTGAAAGCTTC	443						
Oy	1599	C 1599							
Db	442	C 442							
RESULT 5									
BF552757			373 bp	mRNA	Linear	EST 12-DEC-2000			
LOCUS	UI-R-C0-12-d-02-0-UI.r1	UI-R-C0	Rattus norvegicus	cDNA	clone				
DEFINITION	UI-R-C0-12-d-02-0-UI 5', mRNA sequence.								
VERSION	BF552757								
KEYWORDS	BF552757.1	GI:11662487							
SOURCE	EST.								
ORGANISM	Norway rat.								
	Rattus norvegicus								
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;								
	Rattus.								
REFERENCE	1 (bases 1 to 373)								
AUTHORS	Bonaldo,M.F., Lennon,G. and Soares,M.B.								
TITLE	Normalization and subtraction: two approaches to facilitate gene discovery								
JOURNAL	Genome Res. 6 (9), 791-806 (1996)								
MEDLINE	97044477								
COMMENT	Contact: Soares, MB Program for Rat Gene Discovery and Mapping University of Iowa 451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250 Fax: 319 335 9565 Email: msoares@blue.weeg.iowa.edu cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) This clone is also available through the I.M.A.G.E. Consortium at LMLL (linfo@image.llnl.gov). IMAGE ID= 1782759 Seq primer: M13 Forward.								
FEATURES									
SOURCE	Location/Qualifiers								
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	/strain="Sprague-Dawley"								
	/db_xref="taxon:10116"								
	/clone="UI-R-C0-12-d-02-0-UI"								
	/clone_lib="UI-R-C0"								
	/dex_stage="adult"								
	/lab_host="DH10B (Life Technologies)"								
	/note="Vector: pRT3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-C0 library is a subtracted library derived from the UI-R-A1 and UI-R-E1 libraries. The UI-R-A1 library consisted of a mixture of individually tagged normalized libraries constructed from rat placenta, adult lung, brain, liver, kidney, heart, spleen, ovary, and muscle. The UI-R-E1 library consisted of a mixture of individually tagged normalized libraries constructed from 8, 12 and 18-day embryo. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dT track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-C0) was constructed as follows: PCR amplified cDNA inserts from a pool of UI-R-A1 and UI-R-E1 clones from which 3' ESTs had been derived was used as a driver in a hybridization with the pooled UI-R-A1 and UI-R-E1 library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B								

BASE COUNT	106 a	93 c	89 g	85 t			
ORIGIN							
Query Match	11.7% ; Score 187.6; DB 12: Length 373;						
Best Local Similarity	69.2% ; Pred. No. 1,3e-40;						
Matches 256; Conservative	0; Mismatches 114; Indels 0; Gaps 0;						
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Db 4							
	GAGGTGCTGGCTACTATAAGAGACTCTTCCATATATAGAGGAGGACTCTGCTCCACA	63					
QY 1284	AAAGGCCCTTTTATGACAGGTCCTGCTTACGACGACTTATATGAGACTTGAAATCTA	1343					
Db 64							
	AAAGACTCTTTGATGATGAGACCCCTGGCTTGGATGACATATAGAGGACTTGAAGATCTA	123					
QY 1344	CCAGATGGAAATTCAGAGCCATGAGACGCAAAAGCTTTTAAATGATCCCAAGAGGAGATCTT	1403					
Db 124	CCAGTCAGAGTTTCCAGAGGCATTAATATGACAGCACTTCAGAGCCACAATCATATCAGAGATCAC	183					
QY 1404	TCTGTGATTAAGAAACATGCTGACAGCTATGATGAGAGCTGTTACAGGCCCTGAAATTTCAACAG	1463					
Db 184							
	TCTGTGAGAAACATATGCTGATGAGTATGATGAGAGCTAATGCGGCTCTGAATCATCACAGGG	243					
QY 1464	TGTGACTGTGGCACAGAAATCTCCCTTGAGAGAGCGGATTTTATTAACATAAATCAA	1523					
Db 244							
	CGAGATTTCTGCACAGAAAGCTCCCATATGAGAAACAGATCTTACAGAGATGAAATGAA	303					
QY 1544	GCTCTGCATCTCTTCTTCATGCTTTTCAGATTCGTGCGGTACCATCAATAGATGATGTC	1583					
Db 304							
	GCTCTGTATCTCTGCTCCATGCCCTTCAGACACAGCGCTCATGACTATCAACAGGATGATGAA	363					
QY 1584	CTACTTGTAC	1593					
Db 364							
	CTATCTGAGC	373					
RESULT 6							
LOCUS	AZ441303	535 bp	DNA	linear			
DEFINITION	IM0232M2R Mouse 10kb plasmid U00C1M library Mus musculus genomic						
ACCESSION	AZ441303						
VERSION	AZ441303.1						
KEYWORDS	GI:10565316						
SOURCE	house mouse.						
ORGANISM	Mus musculus						
REFERENCE	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi; Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae; Mus. 1 (bases 1 to 535)						
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.						
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts						
JOURNAL	Unpublished (2000)						
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert length: 10000 Std Error: 0.00 Plate: 0232 row: M column: 2A Seq primer: CACACAGAAACACACTATGACC Class: plasmid ends High quality sequence stop: 535.						

B1523569 832 bp mRNA linear EST 29-AUG-2001
 LOCUS B1523569
 DEFINITION 60317593BP1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5240216 5',
 mRNA sequence.
 ACCESSION B1523569
 VERSION B1523569.1 GI:15348361
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 832)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: rsraus@rmail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: L1AM1605 row: 1 column: 09
 High quality sequence start: 23
 High quality sequence stop: 821.
 Location/Qualifiers
 1..832
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone IMAGE:5240216"
 /clone_lib="NIH_MGC_121"
 /lab_host="DH10B"
 /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: EcoRV (destroyed); RNA source anonymous pool of 3
 fetal brains, female age 20 weeks, female age 24 weeks,
 and male age 26 weeks. Library is oligo-dT primed and
 directionally cloned (EcoRV site is destroyed upon
 cloning). Average insert size 1.7 kb, insert size range
 0.7-3.5 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 017. Note:
 this is a NIH-MGC Library."
 BASE COUNT 220 a 233 c 200 g 179 t
 ORIGIN
 Query Match 9.9% Score 157.8; DB 13; Length 832;
 Best Local Similarity 84.7%; Pred. No. 2.9e-32;
 Matches 177; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
 Oy 1010 GAACCTGCGCAACCCCTACTCCATCCCGGATGTTTGAACACCTCCCAA 1069
 ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
 Db 389 GAACCTGCGCGCTGCGCACTCCAGACGAGAAATGTTCCATGCGCTCCCA 448
 Oy 1070 CCTTGTGAGAGCGCTGCGCAACAGCTTGCAGAGCCGACAGAACTAGATTAT 1129
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 449 ACCTGCTGAGGGCGCTGCGCAACATGCTCAGAAAGCCAGACAACTAGATTAT 508
 Oy 1130 CCTGACTTCCGAGAGATTGATCATGAAGATATCAAAAGGATAAACACAGACAGGG 1189
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 509 CTTGACTTCTGAGAGATTGATCATGAAGATATCACAAGATATAAACACAGACAGTGG 568
 Oy 1190 AGGCTGCTTACACATGAATTAAACATG 1218
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 569 AGGCTGCTTACATGAATTAAACATG 597
 RESULT 9
 AG079702 668 bp DNA linear GSS 03-NOV-2001
 LOCUS AG079702
 DEFINITION Pan troglodytes DNA, clone: PTB-075107.R, genomic survey sequence.
 ACCESSION AG079702

VERSION AG079702.1 GI:16631504
 KEYWORDS GSS.
 SOURCE Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
 BAC Library clone:PTB-075107.R.
 ORGANISM Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Pan.
 REFERENCE 1
 AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
 Tokokl,Y., Watanabe,H. and Sakaki,Y.
 TITLE BAC end sequences of library PTB
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 668)
 AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
 Tokokl,Y., Watanabe,H. and Sakaki,Y.
 TITLE Direct Submission
 JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
 1-7-22 Suenho-chou,Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan
 (E-mail:chimbases@gsc.riken.go.jp; URL:<http://hgp.gsc.riken.go.jp/>,
 Tel:81-45-503-9111, Fax:81-45-503-9170)
 Clones are derived from the chimpanzee BAC library PTB This BAC end
 was generated during the Rad process and may have higher chance of
 clone tracking errors.
 PRIMERS
 Sequencing: M13rev
 LIBRARY
 Vector : pRS145
 R.Site 1 : SacI
 R.Site 2 : SacI.
 Location/Qualifiers
 1..668
 /organism="Pan troglodytes"
 /db_xref="taxon:9598"
 /clone="PTB-075107.R"
 /sex="male"
 /cell_type="lymphoblast"
 /clone_lib="PTB Chimpanzee Male BAC Library"
 BASE COUNT 180 a 138 c 137 g 213 t
 ORIGIN
 Query Match 5.9% Score 93.6; DB 17; Length 668;
 Best Local Similarity 79.3%; Pred. No. 1.4e-14;
 Matches 111; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
 Oy 345 TATCTTAAGAGCAGGAAGATCCAAAATAAGATCTTTCGAAGATGAGGACCAAGAA 404
 ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
 Db 561 TTTGTTTATTTCAATTCAGAAACCGAGCTTACACCTTTGTAAGATGCGACACCAAGAA 502
 Oy 405 TTATCTGAGCGTTTCACATGCTGCTGCGTACGCGCAATCAGTACTGATTGAATTTCAG 464
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 501 TTATCAGAGCGTTTCACCTGCTGCTGCTGACGCAATCAGTACTGATTGACTTCAG 442
 Oy 465 TGTCAAGTGCAGAGGCT 484
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 441 TGTCAAGCAGCAGAGGCT 422
 RESULT 10
 BM257856 342 bp mRNA linear EST 17-DEC-2001
 LOCUS BM257856
 DEFINITION 521721 MRC 3BOV Bos taurus cDNA 5', mRNA sequence.
 ACCESSION BM257856
 VERSION BM257856.1 GI:17893455
 KEYWORDS EST.
 SOURCE cow.
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
 Bovidae; Bovinae; Bos.
 REFERENCE 1 (bases 1 to 342)
 AUTHORS Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
 Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett

TITLE
JOURNAL MEDLINE
Contact: Smith TPI
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4365
Fax: 402 762 4360
Email: smithemail@marc.usda.gov
Single pass sequencing. Bases called and all trimmed with phred v0.980504.e. Vector identified by cross_match with the minuscore 18 and -minmatch 12 options.
Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle genome Res. 11 (4), 526-530 (2001)

FEATURES
source
1..342
/organism="Bos laurus"
/db_xref="taxon:9913"
/clone_lib="MARC 3B0Y"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPOR16; Site_1: NotI; Site_2: SalI; Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendinosus muscle, and fetal longissimus muscle."
Seq primer: ATTAGCTGACACTATAG.
Location/Qualifiers

BASE COUNT
ORIGIN
67 a 135 c 74 g 56 t

Query Match
Best Local Similarity 75.5%; Score 73.4; DB 13; Length 342;
Matches 105; Conservative 0; Mismatches 31; Indels 3; Gaps 1;

QY 1009 AGAAGCTTCCAGACCCCTGATTCATCCCGGCTATGTCATGTTTGACAGCCTCCCAA 1068
DB 207 AGGAGCTTCCAGACCCCTGATTCATCCCGGCTATGTCATGTTTGACAGCCTCCCAA 263
QY 1069 ACCTGTGTGAGAGCGCTGACGACAGCGCTTGAAGGCTGACAGCACTGTACAATTATAT 1128
DB 264 AAGCTGTGAGAGCGCTGACGACAGCGCTTGAAGGCTGACAGCACTGTACAATTATAT 323
QY 1129 TCGTCACCTTCGAGAGAGA 1147
DB 324 TCGTCACCTTCGAGAGAGA 342

RESULT 11
B1824638 447 bp mRNA linear EST 04-OCT-2001
LOCUS 60303558001 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5175018 5',
DEFINITION mRNA sequence.
ACCESSION B1824638
VERSION B1824638.1 GI:15936188
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Mammalia: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NIH-MGC http://mgs.mcl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs.fda.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM11435 row: 0 column: 19
High quality sequence start: 3
High quality sequence stop: 445.

FEATURES
source

1..447
Location/Qualifiers

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NIH_MGC_115"
/lab_host="DH10B"
/note="Organ: pooled brain, lung, testis; Vector: pCMV-SPOR16; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH-MGC Library."
BASE COUNT
ORIGIN
149 a 63 c 87 g 148 t

Query Match
Best Local Similarity 85.7%; Score 64.8; DB 13; Length 447;
Matches 72; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1516 AAAATCAAGCTGCTGATCTTTCATGCTTTCACAAATTCGTCGCGTACACCTCATAGA 1575
DB 1 AAAATCAAGCTGCTGATCTTTCATGCTTTCACAAATTCGTCGCGTACACCTCATAGA 60
QY 1576 ATGATGCTCTACTGACCTCTCC 1599
DB 61 GTGATGACGTATCTGATGCTCTCC 84

RESULT 12
A0981401/C 324 bp DNA linear GSS 29-JAN-2000
LOCUS A0981401
DEFINITION RPCT-23-304012.TV RPCT-23 Mus musculus genomic clone RPCT-23-304012
ACCESSION A0981401
VERSION A0981401.1 GI:6813702
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Mammalia: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Zhao,S., Nierman,W., Feldblum,T., Malek,J., Shalzman,S., Akintel, R., Levins,M., McGinn,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCT-23
unpublished (1999)
Other_GSSs: RPCT-23-304012.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhaod@igf.org
Clones are derived from the mouse BAC library RPCT-23. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.html) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 304 row: 0 column: 12

RESULT	15
LOCUS	AA004891
DEFINITION	540 bp mRNA linear EST 07-MAY-1997
ACCESSION	Z676927.1 Soares_fetal_liver_spleen_infls-s1 homo sapiens cDNA
VERSION	clone IMAGE:428305.5, mRNA sequence.
KEYWORDS	AA004891 AA004891 GI:143556
SOURCE	EST.
ORGANISM	human. Homo sapiens

Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.jhu.edu) for further information.
Insert Length: 1150 Std Error: 0.00
Seq primer: mob, BECA-FR
High quality sequence stop: 460.
Location/Qualifiers
1..540

```

(Pharmacia), digested with Pac I and cloned into the Pac
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Felima Bonaldo."
BASE COUNT      148 a      103 c      129 g      154 t      6 others
ORIGIN
Query Match      2.6%; Score 41.6; DB 5; Length 540;
Best Local Similarity 52.7%; Pred. No. 2.9;
Matches 89; Conservative 0; Mismatches 80; Indels 0; Gaps 0;
QY      314  ACMAAAGAGATGCAATTTGGTCCACTGATATCTTAAGGAGACAGAAAGATCCAAA 373
      || || | | | | | | | | | | | | | | | | | | | |
DB      101  ACTGACTGTGCGAAGGAATAGCCGCTTGATAGTAGTGAAGTAAAGACAGGAA 160
QY      374  ATAAAGATCTTCTGAAATGTGAGGCAAGAAATTTATCTGACGTTTCACATGCTGGTGC 433
      || || | | | | | | | | | | | | | | | | | | | |
DB      161  AAAATTCCTCTTTTATTTGGTTCCAAAGAAACCAACCAACCAAGCTCTTGATGT 220
QY      434  TGACCGCATCAGTACGTGATTTGAAATTCAGTGTCAAAAGTAGCAGAG 482
      | || | | | | | | | | | | | | | | | | | | |
DB      221  GAAGATAAATATAGTCTTTTGAATGAGAGGAAAAAGTGGGAGG 269

Search completed: January 14, 2003, 23:46:39
Job time : 1936 secs

```


GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 21, 2003, 15:01:33 : Search time 2846 Seconds

(without alignments)
16351.155 Million cell updates/sec

Title: US-09-917-265-61

Perfect score: 1599
Sequence: 1 atgacacctcgcagcagctggtl.....tgctctacttgaactcttcc 1599

Scoring table: OLI60_NUC

Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Ord size : 0

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: listing first 1000 summaries

Database :

(GenEmbl):
1: gb_ba:*
2: gb_hlg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sls:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_jm:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sls:*
28: em_sy:*
29: em_vl:*
30: em_hlg_hum:*
31: em_hlg_inv:*
32: em_hlg_mus:*
33: em_hlg_mus:*
34: em_hlg_pln:*
35: em_hlg_rnd:*
36: em_hlg_wam:*
37: em_hlg_vrl:*
38: em_sy:*
39: em_hlgo_hum:*
40: em_hlgo_mus:*
41: em_hlgo_other:*

pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	974	60.9	990	6	ARI51071
2	974	60.9	990	6	E15017
3	814	50.9	1015	4	CFU49100
4	798	49.9	990	6	ARI51061
5	580	36.3	588	4	AP349536
6	494	30.9	669	6	ARI51072
7	494	30.9	669	6	E15018
8	444	27.8	452	4	AF333121
9	443	27.7	669	6	ARI51062
10	389	24.3	669	6	CFU49085
11	387	24.2	446	4	AF091134
12	143	8.9	990	6	AX154603
13	128	8.0	984	6	AX154599
14	95	5.9	984	6	AX154600
15	81	5.1	285	4	AF054605
16	81	5.1	669	4	FCU83185
17	81	5.1	669	4	FCU83184
18	75	4.7	666	6	AX154613
19	75	4.7	969	6	AX154601
20	72	4.5	975	6	AX154597
21	66	4.1	431	4	AF054607
22	66	4.1	666	6	AX154612
23	66	4.1	990	4	FCU83184
24	66	4.1	990	6	AX076200
25	66	4.1	990	6	AX076482
26	66	4.1	1006	4	FCU112P40
27	66	4.1	4522	6	AX076209
28	66	4.1	4522	6	AX076476
29	66	3.9	660	6	AX154615
30	62	3.9	660	6	AX154616
31	60	3.8	640	6	E32843
32	59	3.7	660	6	AR008951
33	59	3.7	660	6	AX154614
34	59	3.7	660	6	AX154617
35	59	3.7	660	6	AX154618
36	59	3.7	660	6	AX154619
37	59	3.7	660	6	AX154621
38	59	3.7	660	6	AX154634
39	59	3.7	660	6	BD007071
40	59	3.7	660	6	BD007079
41	59	3.7	660	6	I28592
42	59	3.7	721	6	AR052862
43	59	3.7	762	9	AF101062
44	59	3.7	780	9	MMU19842
45	59	3.7	823	9	AF180562
46	59	3.7	1026	6	AR091390
47	59	3.7	1026	9	HUMCLMF35
48	59	3.7	1287	6	AX084108
49	59	3.7	1316	6	AR050785
50	59	3.7	1316	6	AR212036
51	59	3.7	1316	9	HUMNKSFP35
52	59	3.7	1364	6	AR082685
53	59	3.7	1364	6	AR122961
54	59	3.7	1364	6	I28326
55	59	3.7	1364	6	I89771
56	59	3.7	1560	6	AR091395
57	59	3.7	1623	6	AR091394
58	59	3.7	1645	6	A92078
59	59	3.7	6139	6	AR091393
60	59	3.7	11792	9	AF040773
61	59	3.7	157079	9	AC010370
62	59	3.7	176108	9	AC026118
63	59	3.7	275547	2	AC129109
64	56	3.5	669	6	AX076201
65	56	3.5	669	6	AX076483

66	3.5	4201	6	AX076477	AX076477 Sequence	139	26	1.6	1062	10	AF288612	AF288612 Meriones
56	3.3	786	9	CTU19835	U19835 Cercopithecus	140	25	1.6	71	6	AX076207	AX076207 Sequence
52	3.1	1058	4	EC112P40	V11129 Equus caball	141	24	1.5	39	6	ARI51073	ARI51073 Sequence
68	3.1	1626	12	AF401989	AF401989 Synthetic	142	24	1.5	39	6	E15027	E15027 PCR primer
69	2.9	1005	9	CTU19834	U19834 Cercopithecus	143	24	1.5	987	6	BD007077	BD007077 Gene expr
70	2.9	1080	9	MMU19841	U19841 Macaca mulia	144	24	1.5	987	6	BD007078	BD007078 Gene expr
47	2.9	975	6	AX154602	AX154602 Sequence	145	23	1.4	666	10	AB025723	AB025723 Cavia por
72	2.9	987	6	AR008950	AR008950 Sequence	146	23	1.4	1119	10	AF288849	AF288849 Meriones
46	2.9	987	6	AX154633	AX154633 Sequence	147	23	1.4	1947	6	AX073936	AX073936 Sequence
74	2.9	987	6	BD007070	BD007070 IL-12 gen	148	23	1.4	182791	2	AC112100	AC112100 Rattus no
75	2.9	987	6	BD007076	BD007076 Gene expr	149	23	1.4	240514	10	AL669858	AL669858 Mouse DNA
76	2.9	987	6	128591	I28591 Sequence 1	150	22	1.4	399	10	AF046211	AF046211 Mesocric
77	2.9	1007	6	AF180563	AF180563 Homo sapi	151	22	1.4	149800	2	AC094950	AC094950 Rattus no
78	2.9	1018	6	AR052857	AR052857 Sequence	152	22	1.4	227757	2	AC020706	AC020706 Homo sapi
79	2.9	1389	6	AX084106	AX084106 Sequence	153	21	1.3	76	6	AX076205	AX076205 Sequence
80	2.9	1399	6	AR091391	AR091391 Sequence	154	21	1.3	76	6	AX076208	AX076208 Sequence
81	2.9	1399	6	HUMCMP40	MS5272 Human cytot	155	21	1.3	1425	10	AF421395	AF421395 Sigmodon
82	2.9	1870	6	A92079	A92079 Sequence 3	156	21	1.3	2753	5	XELXGFR42	XELXGFR42
83	2.9	2318	9	HUMNKSPP40	MS5290 Human natur	157	21	1.3	3634	5	XLU2491	XLU2491 Xenopus lae
84	2.9	2362	6	AR082684	AR082684 Sequence	158	21	1.3	3815	5	XELXJFGR	XELXJFGR Xenopus lae
46	2.9	2362	6	ARI22960	ARI22960 Sequence 1	159	21	1.3	7071	4	BTDESMOG1	BTDESMOG1 B.taurus mr
86	2.9	2362	6	128335	I28335 Sequence 1	160	21	1.3	7300	4	BTDESMOG	BTDESMOG Bovine mRNA
87	2.9	2362	6	189770	I89770 Sequence 1	161	21	1.3	119958	2	AC104706	AC104706 Oryza sat
88	2.9	2362	6	AF512686	AF512686 Homo sapi	162	21	1.3	130116	2	AL355792	AL355792 Human DNA
89	2.9	18340	9	AY008847	AY008847 Homo sapi	163	21	1.3	144034	2	AC069244	AC069244 Homo sapi
90	2.9	108511	9	AC011418	AC011418 Homo sapi	164	21	1.3	150614	2	AC126757	AC126757 Homo sapi
91	2.8	525	4	CEU01060	CEU01060 Cervus elap	165	21	1.3	164049	2	AC126753	AC126753 Homo sapi
92	2.8	984	4	AF004024	AF004024 Ovis arie	166	21	1.3	169089	9	AC055725	AC055725 Homo sapi
93	2.8	984	4	AF209435	AF209435 Ovis arie	167	21	1.3	170367	9	AC012469	AC012469 Homo sapi
44	2.8	993	4	CEU57752	U57752 Cervus elap	168	21	1.3	178361	10	AL645471	AL645471 Mouse DNA
95	2.8	1012	4	AF007576	AF007576 Capra hlr	169	21	1.3	179245	9	HUAC002492	HUAC002492 Human Chr
96	2.8	1012	4	BTU11815	U11815 Bos taurus	170	21	1.3	185026	9	AC008785	AC008785 Homo sapi
97	2.8	1019	6	E35794	E35794 Process for	171	21	1.3	192387	9	CNS01DVO	CNS01DVO Human chr
44	2.7	660	6	AX154620	AX154620 Sequence	172	21	1.3	196753	2	AC121598	AC121598 Mus muscu
99	2.6	669	4	EC112P35	V11130 Equus caball	173	21	1.3	211723	2	CNS0000C	CNS0000C Human chr
100	2.2	1426	4	SSU08317	L35765 Sus scrofa	174	21	1.3	300917	2	AC122241	AC122241 Mus muscu
101	2.2	2090	4	AX154598	AX154598 Marmota m	175	20	1.3	20	6	A56994	A56994 Sequence 52
102	2.1	984	6	AX154598	AX154598 Marmota m	176	20	1.3	20	6	AR212061	AR212061 Sequence
103	2.1	984	6	AX154598	AX154598 Marmota m	177	20	1.3	20	6	AR212064	AR212064 Sequence
104	2.1	984	6	AX154598	AX154598 Marmota m	178	20	1.3	20	6	AR212091	AR212091 Sequence
105	2.1	984	6	AX154598	AX154598 Marmota m	179	20	1.3	39	6	ARI51074	ARI51074 Sequence
106	1.9	582	6	AX084103	AX084103 Sequence	180	20	1.3	39	6	E15028	E15028 PCR primer
107	1.9	660	6	E26662	E26662 Improved me	181	20	1.3	73	6	AX268996	AX268996 Sequence
108	1.9	700	10	S82412S4	S82418 Interleukin	182	20	1.3	600	6	E26663	E26663 Improved me
109	1.9	713	10	AR069652	AR069652 Sequence	183	20	1.3	1000	10	S82420S3	S82420 Interleukin
110	1.9	713	10	AF128212	AF128212 Mus muscu	184	20	1.3	1061	6	AR069654	AR069654 Sequence
111	1.9	713	10	AF128213	AF128213 Mus muscu	185	20	1.3	1143	10	AF128214	AF128214 Mus muscu
112	1.9	786	10	AF128210	AF128210 Mus muscu	186	20	1.3	1143	10	AF128215	AF128215 Mus muscu
113	1.9	786	10	AF128211	AF128211 Mus muscu	187	20	1.3	1409	6	AX084105	AX084105 Sequence
114	1.9	827	10	AF421396	AF421396 Sigmodon	188	20	1.3	1472	6	AX084104	AX084104 Sequence
31	1.9	1265	10	MUS1135A	M86672 Mus musculu	189	20	1.3	2616	8	AY050369	AY050369 Arabidops
115	1.9	1278	6	AX084107	AX084107 Sequence	190	20	1.3	3425	3	DMU58282	DMU58282 Drosophila
116	1.9	1569	6	AX084114	AX084114 Sequence	191	20	1.3	3536	8	ANP4A	ANP4A R.nidulans
117	1.9	1669	12	AF411293	AF411293 Synthetic	192	20	1.3	10158	1	AE008944	AE008944 Agrobacte
118	1.9	2013	6	AX084115	AX084115 Sequence	193	20	1.3	11612	1	AE007892	AE007892 Agrobacte
119	1.9	2709	6	AX084115	AX084115 Sequence	194	20	1.3	25214	2	AC016930	AC016930 Homo sapi
120	1.9	528	10	AF082494	AF082494 Marmota m	195	20	1.3	56689	2	AC119966	AC119966 Mus muscu
121	1.9	528	10	AF082494	AF082494 Marmota m	196	20	1.3	76047	10	AL669944	AL669944 Mouse DNA
122	1.9	528	10	AF082494	AF082494 Marmota m	197	20	1.3	85109	8	ATT2213	ATT2213 Arabidops
123	1.9	793	10	AF177031	AF177031 Rattus no	198	20	1.3	85322	8	AL138923	AL138923 Human DNA
124	1.9	793	10	AF177031	AF177031 Rattus no	199	20	1.3	89942	3	AC005149	AC005149 Drosophila
125	1.9	666	4	AF173557	AF173557 Ovis arie	200	20	1.3	100496	2	AC114277	AC114277 Homo sapi
126	1.8	690	4	AF003542	U14416 Bos taurus	201	20	1.3	101140	2	AC020022	AC020022 Drosophila
127	1.8	690	4	AF003542	E35793 Process for	202	20	1.3	101243	2	AC117458	AC117458 Homo sapi
128	1.8	703	6	E35793	A1771034 Bos tauru	203	20	1.3	101789	9	AL161659	AL161659 Human DNA
129	1.8	711	4	OKR271034	A1771035 Ovis arie	204	20	1.3	105081	2	AC026439	AC026439 Homo sapi
130	1.8	714	4	OKR271035	AC092942 Homo sapi	205	20	1.3	106525	2	AP004017	AP004017 Oryza sat
131	1.8	288652	2	AC092942	S82489 Interleukin	206	20	1.3	108393	8	AC005315	AC005315 Arabidops
132	1.7	335	10	AF288520	AF288520 Marmota m	207	20	1.3	110000	2	AC073744	AC073744 Oryza sat
133	1.7	672	10	MMIL12P35	X97018 M.momax mrn	208	20	1.3	120029	2	HSJ282H10	HSJ282H10 Continuation (4 of
134	1.7	672	10	MMIL12P35	U16674 Rattus norv	209	20	1.3	120029	2	HSJ282H10	HSJ282H10 Continuation (4 of
135	1.7	821	10	RNU16674	U16674 Rattus norv	210	20	1.3	126189	9	AC008807	AC008807 Homo sapi
136	1.7	1008	10	AF133197	U57751 Cervus elap	211	20	1.3	126189	9	AC008807	AC008807 Homo sapi
137	1.6	666	4	CEU57751	U57751 Cervus elap	211	20	1.3	126189	9	AC008807	AC008807 Homo sapi
138	1.6	666	4	CEU57751	U57751 Cervus elap	211	20	1.3	126189	9	AC008807	AC008807 Homo sapi

212	20	1.3	138593	2	AP005190	Oryza sat	285	19	1.2	1766	10	MMPGIM3M	X65083 M.musculus
213	20	1.3	140325	2	AC128875	Rattus no	286	19	1.2	1831	14	HCUS7431	U57431 Human cytom
C 214	20	1.3	144583	2	AP004793	AP004793 Oryza sat	C 287	19	1.2	1840	13	AB052656	AB052656 Mytilus g
C 215	20	1.3	146208	9	AL354776	AL354776 Human DNA	C 288	19	1.2	1939	14	HCUS7434	U57434 Human cytom
C 216	20	1.3	147622	2	AC110437	AC110437 Rattus no	C 289	19	1.2	1997	10	MMPGIM4M	AK097804 M.musculus
C 217	20	1.3	148189	9	AC018796	AC018796 Homo sapi	C 290	19	1.2	2041	9	AK097804	AK097804 Homo sapi
C 218	20	1.3	149569	2	AC024180	AC024180 Homo sapi	C 291	19	1.2	2114	10	AF283518	AF283518 Mus muscu
C 219	20	1.3	150084	2	AC117653	AC117653 Mus muscu	C 292	19	1.2	2124	10	AF268871	AF268871 Mus muscu
C 220	20	1.3	151549	9	AC092664	AC092664 Homo sapi	C 293	19	1.2	2129	10	RATNF1AB	D78018 Rat mRNA fo
C 221	20	1.3	152770	9	AL359713	AL359713 Homo sapi	C 294	19	1.2	2131	10	BC024915	BC024915 Mus muscu
C 222	20	1.3	152966	9	AL359713	AL359713 Human DNA	C 295	19	1.2	2193	5	AY070267	AY070267 Danio rer
C 223	20	1.3	157023	2	AC013625	AC013625 Homo sapi	C 296	19	1.2	2200	10	RATNF1AA	D78017 Rat mRNA fo
C 224	20	1.3	164775	2	AC114901	AC114901 Mus muscu	C 297	19	1.2	2253	14	HCUS7432	U57432 Human cytom
C 225	20	1.3	167021	2	AC093187	AC093187 Rattus no	C 298	19	1.2	2266	6	AR073028	AR073028 Sequence
C 226	20	1.3	167289	2	AC093187	AC093187 Papio cyn	C 299	19	1.2	2266	6	AR073028	AR073028 Sequence
C 227	20	1.3	171800	2	AC119310	AC119310 Rattus no	C 300	19	1.2	2266	6	HOMELK1A	M55269 Homo sapien
C 228	20	1.3	172537	2	AC073122	AC073122 Homo sapi	C 301	19	1.2	2290	14	HCUS7433	U57433 Human cytom
C 229	20	1.3	173303	9	AC117456	AC117456 Homo sapi	C 302	19	1.2	2520	14	HS51E5KB1	S80870 BETA3-class
C 230	20	1.3	174672	9	AC039057	AC039057 Homo sapi	C 303	19	1.2	2590	10	MM0251594	AJ251594 Mus muscu
C 231	20	1.3	176850	2	AC103736	AC103736 Homo sapi	C 304	19	1.2	2613	10	AF042783	AF042783 Mus muscu
C 232	20	1.3	177153	9	AC100786	AC100786 Homo sapi	C 305	19	1.2	2794	10	AF042783	AF042783 Mus muscu
C 233	20	1.3	179406	2	AC016344	AC016344 Homo sapi	C 306	19	1.2	2848	3	AF332551	AF332551 Bombyx mo
C 234	20	1.3	181825	2	AC068191	AC068191 Homo sapi	C 307	19	1.2	2936	3	AB046691	AB046691 Sarcophag
C 235	20	1.3	184090	2	AC009564	AC009564 Homo sapi	C 308	19	1.2	3030	8	VCA429230	AJ429230 Volvox ca
C 236	20	1.3	187110	2	AC084624	AC084624 Homo sapi	C 309	19	1.2	3058	6	AR129249	AR129249 Sequence
C 237	20	1.3	187707	2	AC092240	AC092240 Drosophil	C 310	19	1.2	3127	6	AX239635	AX239635 Sequence
C 238	20	1.3	187740	3	AC126863	AC126863 Rattus no	C 311	19	1.2	3150	10	AB060652	AB060652 Rattus no
C 239	20	1.3	189236	10	AL607030	AL607030 Mouse DNA	C 312	19	1.2	3164	10	RATMET1A	M61874 Rattus norv
C 240	20	1.3	192100	9	AC021810	AC021810 Homo sapi	C 313	19	1.2	3207	6	A30543	AB0543 Rattus norv
C 241	20	1.3	193360	9	AC021977	AC021977 Homo sapi	C 314	19	1.2	3207	6	119505	AB0543 Rattus norv
C 242	20	1.3	195290	9	AL354795	AL354795 Human DNA	C 315	19	1.2	3276	10	RNFNF1A	I19505 Sequence 1
C 243	20	1.3	197245	2	AL591164	AL591164 Homo sapi	C 316	19	1.2	3350	10	AF112455	X84210 R.norvegicu
C 244	20	1.3	198764	9	AC103805	AC103805 Homo sapi	C 317	19	1.2	3368	10	RNFNF1	AF112455 Rattus no
C 245	20	1.3	200340	9	AC009597	AC009597 Homo sapi	C 318	19	1.2	3772	3	AY119139	X84209 R.norvegicu
C 246	20	1.3	214523	2	AC103681	AC103681 Homo sapi	C 319	19	1.2	4034	3	AF384554	AY119139 Drosophil
C 247	20	1.3	215514	2	AC040582	AC040582 Mus muscu	C 320	19	1.2	4034	10	RNU65138	AF384554 Plasmodu
C 248	20	1.3	221712	2	AC126447	AC126447 Mus muscu	C 321	19	1.2	4138	3	AF332918	AF332918 Plasmodu
C 249	20	1.3	247794	2	AC126044	AC126044 Mus muscu	C 322	19	1.2	4138	3	AF506832	AF506832 Plasmodu
C 250	20	1.3	256841	2	AC127284	AC127284 Mus muscu	C 323	19	1.2	4138	3	AF506833	AF506833 Plasmodu
C 251	20	1.3	259259	2	AC114558	AC114558 Mus muscu	C 324	19	1.2	4138	3	AF506834	AF506834 Plasmodu
C 252	20	1.3	268294	2	AC020085	AC020085 Mus muscu	C 325	19	1.2	4138	3	AY099885	AY099885 Plasmodu
C 253	20	1.3	287927	2	AC079530	AC079530 Mus muscu	C 326	19	1.2	4138	3	AY099887	AY099887 Plasmodu
C 254	20	1.3	295850	1	AC128691	AC128691 Homo sapi	C 327	19	1.2	4138	3	AY099888	AY099888 Plasmodu
C 255	20	1.3	301450	1	AP003188	AP003188 C1orf1d	C 328	19	1.2	4138	3	AY099888	AY099888 Plasmodu
C 256	20	1.3	307748	3	AE003578	AE003578 Drosophil	C 329	19	1.2	4265	9	HSM801471	AY099888 Plasmodu
C 257	19	1.2	20	6	AR212092	AR212092 Sequence	C 330	19	1.2	4704	9	AB023193	AL133612 Homo sapi
C 258	19	1.2	25	6	AR091400	AR091400 Sequence	C 331	19	1.2	4991	7	AF208841	AB023193 Homo sapi
C 259	19	1.2	30	6	E35791	E35791 Process. for	C 332	19	1.2	5000	9	AF334585	AF208841 Bacteriop
C 260	19	1.2	264	9	HS110C4F	Z58657 H.sapiens C	C 333	19	1.2	5236	10	RNU41453	AF334585 Homo sapi
C 261	19	1.2	353	3	LMARKHGEN	X86759 L.migratori	C 334	19	1.2	5517	9	AB040890	U41453 Rattus norv
C 262	19	1.2	423	8	CRFCRGP501	127258 Chlamydomon	C 335	19	1.2	6128	10	AF236130	AB040890 Homo sapi
C 263	19	1.2	510	14	HSSVMYCB	M11098 Human cytom	C 336	19	1.2	6160	10	RNU23146	AF236130 Rattus no
C 264	19	1.2	742	9	AF000672	AF000672 Homo sapi	C 337	19	1.2	7393	4	AB069764	U23146 Rattus norv
C 265	19	1.2	849	4	AB022797	AB022797 Sus scrof	C 338	19	1.2	7764	10	RNU81010	AB069764 Sus scrof
C 266	19	1.2	849	4	AF397407	AF397407 Sus scrof	C 339	19	1.2	10903	1	AB087407	U81010 Rattus norv
C 267	19	1.2	849	4	AY033634	AY033634 Sus scrof	C 340	19	1.2	11514	1	AF486549	AB087407 Bacillus
C 268	19	1.2	937	6	HOMELK1	AF080615 Homo sapi	C 341	19	1.2	11647	3	U41035	AF486549 Campyloba
C 269	19	1.2	1002	6	A26367	A26367 R.norvegicu	C 342	19	1.2	14147	6	AX251502	U41035 Caenorhabdi
C 270	19	1.2	1002	6	AR073455	AR073455 Sequence	C 343	19	1.2	14147	6	AX347393	AX251502 Sequence
C 271	19	1.2	1008	1	AF194025	AF194025 Streptomy	C 344	19	1.2	14147	6	AX349114	AX347393 Sequence
C 272	19	1.2	1083	10	RATNF1AD	D78020 Rat mRNA fo	C 345	19	1.2	17294	6	AX345888	AX349114 Sequence
C 273	19	1.2	1145	3	AF026145	AF026145 Cerealis	C 346	19	1.2	23008	9	AB016194	AX345888 Sequence
C 274	19	1.2	1155	8	AB062905	AB062905 Physcomit	C 347	19	1.2	25231	2	AC015313	AB016194 Homo sapi
C 275	19	1.2	1245	10	MUSACDA4A	LI3611 Mus musculu	C 348	19	1.2	27102	3	CEP22B8	AC015313 Drosophil
C 276	19	1.2	1245	10	MUSACDA4A	X69724 M.musculu	C 349	19	1.2	32688	2	AC014984	CEP22B8 Caenorhabdi
C 277	19	1.2	1258	1	D85897	D85897 Streptomyces	C 350	19	1.2	34688	6	AX458544	AC014984 Drosophil
C 278	19	1.2	1314	10	AF014395	AF014395 Rattus no	C 351	19	1.2	34907	3	AF067624	AX458544 Sequence
C 279	19	1.2	1445	10	RATNF1AC	D78019 Rat mRNA fo	C 352	19	1.2	37482	3	AC024790	AF067624 Caenorhab
C 280	19	1.2	1450	10	RNO297631	LI297631 Rattus no	C 353	19	1.2	38888	2	U41543	AC024790 Caenorhab
C 281	19	1.2	1461	6	AX276325	AX276325 Sequence	C 354	19	1.2	40531	2	AC121128	U41543 Caenorhabdi
C 282	19	1.2	1528	3	CACGCR1A	X1976 D.melanogas	C 355	19	1.2	44190	8	AC109645	AC121128 Mus muscu
C 283	19	1.2	1648	9	HSEIK1	V11432 H.sapiens e	C 356	19	1.2	44222	9	AC008989	AC109645 Oryza sat
C 284	19	1.2	1712	10	RNNP1L	X13167 Rat mRNA fr	C 357	19	1.2	46100	9	AC006126	AC008989 Homo sapi

C 358	19	1.2	48202	2	AC012911	AC012911 Drosophil	C 431	19	1.2	131400	2	AC117642	AC117642 Mus muscu
C 359	19	1.2	48715	6	AX276312	AX276312 Sequence	C 432	19	1.2	131905	2	OSJN00131	AL606995 Oryza sat
C 360	19	1.2	54640	8	AP004316	AP004316 Oryza sat	C 433	19	1.2	131969	2	AC116944	AC116944 Tetradon
C 361	19	1.2	55001	1	AC084290	AC084290 Homo sapi	C 434	19	1.2	133121	8	AC092553	AC092553 Oryza sat
C 362	19	1.2	55593	1	BSA12571	BSA12571 Bacillus	C 435	19	1.2	135129	2	AC123319	AC123319 Rattus no
C 363	19	1.2	62789	2	AC115727	AC115727 Mus muscu	C 436	19	1.2	135302	2	AC130264	AC130264 Rattus no
C 364	19	1.2	62836	2	AC004811	AC004811 Homo sapi	C 437	19	1.2	137724	8	AC122147	AC122147 Oryza sat
C 365	19	1.2	63358	2	AC073448	AC073448 Homo sapi	C 438	19	1.2	138025	8	AP003261	AP003261 Oryza sat
C 366	19	1.2	63377	2	AC116508	AC116508 Mus muscu	C 439	19	1.2	138289	8	AC119771	AC119771 Rattus no
C 367	19	1.2	66128	2	AC126341	AC126341 Homo sapi	C 440	19	1.2	141862	8	AP002913	AP002913 Oryza sat
C 368	19	1.2	67054	2	AC117734	AC117734 Mus muscu	C 441	19	1.2	143568	2	AC117253	AC117253 Rattus no
C 369	19	1.2	67565	2	AC122763	AC122763 Mus muscu	C 442	19	1.2	144821	8	OSJN00146	AL662935 Oryza sat
C 370	19	1.2	68624	2	AC101608	AC101608 Mus muscu	C 443	19	1.2	145472	2	AC096856	AC096856 Oryza sat
C 371	19	1.2	70085	2	AC091419	AC091419 Mus muscu	C 444	19	1.2	145487	8	AC108338	AC108338 Rattus no
C 372	19	1.2	70804	2	AC106273	AC106273 Rattus no	C 445	19	1.2	145744	8	FA14	AF272705 Arabidops
C 373	19	1.2	74697	2	AC020500	AC020500 Drosophil	C 446	19	1.2	145831	6	AX330137	AX330137 Sequence
C 374	19	1.2	76477	2	AC022977	AC022977 Homo sapi	C 447	19	1.2	145831	6	AX334634	AX334634 Sequence
C 375	19	1.2	78483	9	AC098651	AC098651 Homo sapi	C 448	19	1.2	145831	6	AX336416	AX336416 Sequence
C 376	19	1.2	83383	2	AC095331	AC095331 Rattus no	C 449	19	1.2	145831	6	AX337041	AX337041 Sequence
C 377	19	1.2	84344	2	AC105464	AC105464 Rattus no	C 450	19	1.2	145831	8	HUAF001548	AP001548 Human Chr
C 378	19	1.2	89147	2	AC107911	AC107911 Homo sapi	C 451	19	1.2	146081	8	AP001366	AP001366 Oryza sat
C 379	19	1.2	89536	2	OSJN00026	AL606593 Oryza sat	C 452	19	1.2	146568	9	AC105364	AC105364 Oryza sat
C 380	19	1.2	90015	9	AL513264	AL513264 Human DNA	C 453	19	1.2	146921	9	AC007992	AC007992 Homo sapi
C 381	19	1.2	92493	2	AC111396	AC111396 Rattus no	C 454	19	1.2	147207	2	AC078890	AC078890 Oryza sat
C 382	19	1.2	95351	2	AL845299	AL845299 Mus muscu	C 455	19	1.2	147214	2	AC123503	AC123503 Rattus no
C 383	19	1.2	95587	2	AC095820	AC095820 Rattus no	C 456	19	1.2	147395	8	OSJN00014	AL606442 Oryza sat
C 384	19	1.2	96902	9	AC012599	AC012599 Homo sapi	C 457	19	1.2	147862	9	AC079317	AC079317 Homo sapi
C 385	19	1.2	98300	9	AC083790	AC083790 Homo sapi	C 458	19	1.2	147968	2	AC114256	AC114256 Rattus no
C 386	19	1.2	100000	9	AP000077	AP000077 Homo sapi	C 459	19	1.2	148021	10	AL732556	AL732556 Mouse DNA
C 387	19	1.2	100590	8	OSJN000191	AL662991 Oryza sat	C 460	19	1.2	148057	9	AL390035	AL390035 Human DNA
C 388	19	1.2	100996	2	AC096807	AC096807 Rattus no	C 461	19	1.2	148624	2	AC084815	AC084815 Homo sapi
C 389	19	1.2	102822	2	AC097731	AC097731 Rattus no	C 462	19	1.2	149654	8	AC080019	AC080019 Genomic s
C 390	19	1.2	103347	9	AL136086	AL136086 Human DNA	C 463	19	1.2	149884	9	AC016736	AC016736 Homo sapi
C 391	19	1.2	103550	2	AP004003	AP004003 Oryza sat	C 464	19	1.2	150916	2	AC112591	AC112591 Rattus no
C 392	19	1.2	104012	8	AP000861	AP000861 Homo sapi	C 465	19	1.2	151933	2	AC119312	AC119312 Rattus no
C 393	19	1.2	104204	2	ATP9C5	AC123964 Arabidops	C 466	19	1.2	152227	9	AC112220	AC112220 Homo sapi
C 394	19	1.2	104389	9	AC009184	AC009184 Drosophil	C 467	19	1.2	152836	2	AC009171	AC009171 Homo sapi
C 395	19	1.2	104418	2	AC119740	AC119740 Homo sapi	C 468	19	1.2	153087	2	AC017072	AC017072 Homo sapi
C 396	19	1.2	105350	2	AP000661	AP000661 Homo sapi	C 469	19	1.2	153325	2	AC113715	AC113715 Rattus no
C 397	19	1.2	106033	2	AC095853	AC095853 Rattus no	C 470	19	1.2	153414	9	AC093430	AC093430 Homo sapi
C 398	19	1.2	107820	2	CNS08C8J	AL731880 Oryza sat	C 471	19	1.2	153733	3	AC023681	AC023681 Drosophil
C 399	19	1.2	108685	2	AL157383	AL157383 Homo sapi	C 472	19	1.2	153816	2	AC112108	AC112108 Rattus no
C 400	19	1.2	110000	2	AC084288_1	Continuation (2 of	C 473	19	1.2	154011	2	AC018571	AC018571 Homo sapi
C 401	19	1.2	110000	2	CEY39B6_1	Continuation (2 of	C 474	19	1.2	154138	2	AP005108	AP005108 Oryza sat
C 402	19	1.2	110000	2	HSS171M_1	Continuation (2 of	C 475	19	1.2	154594	9	AL161722	AL161722 Human DNA
C 403	19	1.2	110000	2	HSS171M_2	Continuation (3 of	C 476	19	1.2	154909	2	AP005174	AP005174 Oryza sat
C 404	19	1.2	110000	2	LMPLCHR16_00	AL499619 Leishmani	C 477	19	1.2	155797	2	AC073049	AC073049 Homo sapi
C 405	19	1.2	110492	2	AP004139	AP004139 Oryza sat	C 478	19	1.2	156159	8	AC079935	AC079935 Genomic s
C 406	19	1.2	111051	2	AF332449	AF332449 Homo sapi	C 479	19	1.2	156601	9	HS21266	AL009172 Homo sapi
C 407	19	1.2	112746	2	AC130995	AC130995 Rattus no	C 480	19	1.2	156873	9	AC015998	AC015998 Homo sapi
C 408	19	1.2	113328	2	AP003999	AP003999 Oryza sat	C 481	19	1.2	156947	8	OSJN00122	AL606990 Oryza sat
C 409	19	1.2	113862	9	AC104774	AC104774 Homo sapi	C 482	19	1.2	157691	9	AC009051	AC009051 Homo sapi
C 410	19	1.2	116976	9	AC011415	AC011415 Homo sapi	C 483	19	1.2	157750	9	AL512599	AL512599 Human DNA
C 411	19	1.2	117145	9	AC011370	AC011370 Homo sapi	C 484	19	1.2	158136	2	AP005363	AP005363 Homo sapi
C 412	19	1.2	118521	9	AC119049	AC119049 Homo sapi	C 485	19	1.2	158496	2	AC113170	AC113170 Homo sapi
C 413	19	1.2	118521	9	HUAC004514	AC004514 Homo sapi	C 486	19	1.2	158537	2	AC106555	AC106555 Rattus no
C 414	19	1.2	118521	9	AC040159	AC040159 Homo sapi	C 487	19	1.2	158835	2	AC130857	AC130857 Rattus no
C 415	19	1.2	118595	9	AC002379	AC002379 Human BAC	C 488	19	1.2	158868	9	AC113168	AC113168 Homo sapi
C 416	19	1.2	118873	9	HS1184F4	AL034550 Human DNA	C 489	19	1.2	159042	10	AC112163	AC112163 Mus muscu
C 417	19	1.2	119562	2	AC006779	AC006779 Caenorhab	C 490	19	1.2	159264	2	AC092726	AC092726 Homo sapi
C 418	19	1.2	121187	2	AC084308	AC084308 Homo sapi	C 491	19	1.2	159765	2	AC007337	AC007337 Homo sapi
C 419	19	1.2	122032	9	AL513187	AL513187 Human DNA	C 492	19	1.2	159939	2	AC040958	AC040958 Homo sapi
C 420	19	1.2	122789	2	OSJN00101	AL606657 Oryza sat	C 493	19	1.2	160069	2	AC023329	AC023329 Homo sapi
C 421	19	1.2	123057	9	AL1390236	AL1390236 Human DNA	C 494	19	1.2	160174	2	AP005103	AP005103 Oryza sat
C 422	19	1.2	124455	2	AC126886	AC126886 Rattus no	C 495	19	1.2	160589	2	AC113895	AC113895 Rattus no
C 423	19	1.2	126801	9	AC004849	AC004849 Homo sapi	C 496	19	1.2	161067	2	AL607133	AL607133 Homo sapi
C 424	19	1.2	127152	2	AC123898	AC123898 Medicago	C 497	19	1.2	161329	2	AC112344	AC112344 Rattus no
C 425	19	1.2	127524	2	AL807806	AL807806 Mus muscu	C 498	19	1.2	161673	2	AC121695	AC121695 Rattus no
C 426	19	1.2	128396	2	AC034262	AC034262 Homo sapi	C 499	19	1.2	161810	10	AL663086	AL663086 Mouse DNA
C 427	19	1.2	128680	2	AC023374	AC023374 Homo sapi	C 500	19	1.2	162181	2	AC119446	AC119446 Rattus no
C 428	19	1.2	129241	9	AL353660	AL353660 Human DNA	C 501	19	1.2	162317	2	AP005148	AP005148 Oryza sat
C 429	19	1.2	130795	2	AC108875	AC108875 Oryza sat	C 502	19	1.2	162401	2	AC015646	AC015646 Homo sapi
C 430	19	1.2	131300	2	AC116844	AC116844 Mus muscu	C 503	19	1.2	163208	2	AC124923	AC124923 Rattus no

C 504	19	1.2	1.63226	3	AC0090039	Homo sapi	C 577	19	1.2	1.86227	2	AC115463	Rattus no
C 505	19	1.2	1.63710	3	AC0237709	Drosophila	C 578	19	1.2	1.87698	2	AC127951	Rattus no
C 506	19	1.2	1.63856	2	AC0263362	Homo sapi	C 579	19	1.2	1.87931	2	AC073935	Mus muscu
C 507	19	1.2	1.63870	2	AC098149	Rattus no	C 580	19	1.2	1.87994	2	AC126146	Rattus no
C 508	19	1.2	1.64058	2	AC010755	Homo sapi	C 581	19	1.2	1.88073	2	AC130267	Rattus no
C 509	19	1.2	1.65125	2	AC058087	Rattus no	C 582	19	1.2	1.88923	9	AC009267	Homo sapi
C 510	19	1.2	1.65589	9	AL356584	Human DNA	C 583	19	1.2	1.89357	9	AC016642	Homo sapi
C 511	19	1.2	1.66049	2	AC037470	Homo sapi	C 584	19	1.2	1.89671	2	AC067848	Homo sapi
C 512	19	1.2	1.66103	2	CNS08CAC	AL813799	C 585	19	1.2	1.90070	2	AC117160	AL117160 Rattus no
C 513	19	1.2	1.66322	2	AC118913	Rattus no	C 586	19	1.2	1.90289	10	AL732540	Mouse DNA
C 514	19	1.2	1.66335	2	AC073795	Mus muscu	C 587	19	1.2	1.90514	2	AC026363	AC026363 Homo sapi
C 515	19	1.2	1.66801	2	AC103240	Rattus no	C 588	19	1.2	1.90891	2	AC058800	Homo sapi
C 516	19	1.2	1.66974	2	AC046177	Homo sapi	C 589	19	1.2	1.91583	9	AC015651	AC015651 Homo sapi
C 517	19	1.2	1.67258	2	AP004766	Oryza sat	C 590	19	1.2	1.91992	2	AC097815	AC097815 Rattus no
C 518	19	1.2	1.67817	2	AC005842	Homo sapi	C 591	19	1.2	1.92581	2	PFMAL13P1	PFMAL13P1 Plasmodiu
C 519	19	1.2	1.67916	2	AC094048	Rattus no	C 592	19	1.2	1.92585	2	AC015941	AC015941 Homo sapi
C 520	19	1.2	1.67922	2	AC016085	Rattus no	C 593	19	1.2	1.93437	2	AC126667	Rattus no
C 521	19	1.2	1.68242	9	AC020692	Homo sapi	C 594	19	1.2	1.95002	2	AC123812	Mus muscu
C 522	19	1.2	1.68476	2	AC098471	Rattus no	C 595	19	1.2	1.95294	2	AC051623	AC051623 Mus muscu
C 523	19	1.2	1.68764	8	AC087726	Chlamydom	C 596	19	1.2	1.95314	2	AC130746	AC130746 Rattus no
C 524	19	1.2	1.70307	2	CNS10003	AL049777	C 597	19	1.2	1.96067	2	AC068560	AC068560 Mus muscu
C 525	19	1.2	1.70578	2	AC10703	Rattus chr	C 598	19	1.2	1.96604	2	AC127999	Rattus no
C 526	19	1.2	1.70701	2	AC050805	Homo sapi	C 599	19	1.2	1.96649	2	AC109504	AC109504 Mus muscu
C 527	19	1.2	1.71072	2	AP000910	Homo sapi	C 600	19	1.2	1.97248	2	AL844135	AL844135 Mus muscu
C 528	19	1.2	1.71173	2	AF481054	Mus muscu	C 601	19	1.2	1.97650	2	AC027690	AC027690 Homo sapi
C 529	19	1.2	1.71438	8	AP004610	Oryza sat	C 602	19	1.2	1.98043	2	AC123247	AC123247 Rattus no
C 530	19	1.2	1.71744	3	CNS01DM9	AL136520	C 603	19	1.2	1.98043	2	AL173232	AL173232 Mus muscu
C 531	19	1.2	1.72036	9	AC046181	Homo sapi	C 604	19	1.2	1.98444	9	AC018499	AC018499 Homo sapi
C 532	19	1.2	1.72105	3	AC104625	Drosophila	C 605	19	1.2	1.98453	9	AC018502	AC018502 Homo sapi
C 533	19	1.2	1.72175	3	AC010038	Drosophila	C 606	19	1.2	1.99566	9	AC103676	AC103676 Homo sapi
C 534	19	1.2	1.72387	2	AC128718	Rattus no	C 607	19	1.2	1.99595	2	AC107731	AC107731 Mus muscu
C 535	19	1.2	1.73252	9	AC036176	Homo sapi	C 608	19	1.2	1.99847	10	AL691431	AL691431 Mouse DNA
C 536	19	1.2	1.74414	2	AC125291	Drosophila	C 609	19	1.2	1.99985	2	AL353767	AL353767 Homo sapi
C 537	19	1.2	1.74301	2	AP003523	Oryza sat	C 610	19	1.2	2.00092	10	AL731775	Mouse DNA
C 538	19	1.2	1.74533	2	AC073718	Mus muscu	C 611	19	1.2	2.00298	10	AL593858	AL593858 Mouse DNA
C 539	19	1.2	1.74572	2	AL772195	Mus muscu	C 612	19	1.2	2.01371	2	AC008538	AC008538 Homo sapi
C 540	19	1.2	1.75005	2	AP005521	Oryza sat	C 613	19	1.2	2.01371	2	AC073786	AC073786 Mus muscu
C 541	19	1.2	1.75071	2	AC069213	Homo sapi	C 614	19	1.2	2.01371	10	AC096784	AC096784 Mus muscu
C 542	19	1.2	1.76280	2	AC129887	Alelelix	C 615	19	1.2	2.02111	10	AC087061	AC087061 Mus muscu
C 543	19	1.2	1.76280	2	AC129887	Alelelix	C 616	19	1.2	2.02764	10	AL5896570	AL5896570 Mouse DNA
C 544	19	1.2	1.76410	2	AC113085	Mus muscu	C 617	19	1.2	2.03230	10	AC015292	AC015292 Homo sapi
C 545	19	1.2	1.76562	9	AC084864	Mus muscu	C 618	19	1.2	2.03644	2	AC073703	AC073703 Mus muscu
C 546	19	1.2	1.76911	2	AC127678	Mus muscu	C 619	19	1.2	2.07166	2	AC114591	AC114591 Mus muscu
C 547	19	1.2	1.76911	2	AC127678	Mus muscu	C 620	19	1.2	2.07440	2	AC015884	AC015884 Homo sapi
C 548	19	1.2	1.77121	2	AC010955	Homo sapi	C 621	19	1.2	2.07614	2	BSH00008	BSH00008 Homo sapi
C 549	19	1.2	1.77140	2	AP005612	Oryza sat	C 622	19	1.2	2.08230	1	AC093464	AC093464 Mus muscu
C 550	19	1.2	1.77583	3	AC105264	Drosophila	C 623	19	1.2	2.08613	2	AC079262	AC079262 Homo sapi
C 551	19	1.2	1.78413	8	AL805954	Mus muscu	C 624	19	1.2	2.08686	9	AL645584	AL645584 Mus muscu
C 552	19	1.2	1.78692	8	AC024594	Oryza sat	C 625	19	1.2	2.09929	2	AC116572	AC116572 Mus muscu
C 553	19	1.2	1.78954	2	AC115647	Rattus no	C 626	19	1.2	2.0816	2	AC073734	AC073734 Mus muscu
C 554	19	1.2	1.79048	9	AC096642	Homo sapi	C 627	19	1.2	2.10861	2	AC106335	AC106335 Rattus no
C 555	19	1.2	1.79187	9	AC073583	Homo sapi	C 628	19	1.2	2.11868	2	AC079235	AC079235 Homo sapi
C 556	19	1.2	1.79332	2	AC099252	Homo sapi	C 629	19	1.2	2.12327	9	AC112652	AC112652 Homo sapi
C 557	19	1.2	1.79363	3	AC092723	Rattus no	C 630	19	1.2	2.15540	2	AC099790	AC099790 Homo sapi
C 558	19	1.2	1.79517	2	AC026361	Drosophila	C 631	19	1.2	2.14146	2	AC109231	AC109231 Mus muscu
C 559	19	1.2	1.79528	2	AC084862	Papio cyn	C 632	19	1.2	2.14161	2	AC024694	AC024694 Mus muscu
C 560	19	1.2	1.80401	9	AC007489	Homo sapi	C 633	19	1.2	2.15516	1	BSU00007	BSU00007 Homo sapi
C 561	19	1.2	1.80509	9	AC012175	Homo sapi	C 634	19	1.2	2.16750	1	AC117117	AC117117 Rattus no
C 562	19	1.2	1.80627	2	AC121857	Mus muscu	C 635	19	1.2	2.16580	2	AL833772	AL833772 Mus muscu
C 563	19	1.2	1.80658	2	AC023956	Homo sapi	C 636	19	1.2	2.18816	3	AE003451	AE003451 Drosophila
C 564	19	1.2	1.81180	3	AC084248	Homo sapi	C 637	19	1.2	2.20623	2	AL824706	AL824706 Mus muscu
C 565	19	1.2	1.82080	9	AC012373	Drosophila	C 638	19	1.2	2.22492	2	AC109506	AC109506 Mus muscu
C 566	19	1.2	1.82282	9	AC018839	Homo sapi	C 639	19	1.2	2.22233	2	AL807747	AL807747 Mus muscu
C 567	19	1.2	1.83045	9	AC016906	Homo sapi	C 640	19	1.2	2.22326	2	AL162424	AL162424 Human DNA
C 568	19	1.2	1.83721	2	AC128555	Rattus no	C 641	19	1.2	2.23020	9	AC102595	AC102595 Mus muscu
C 569	19	1.2	1.84140	2	AC121475	Rattus no	C 642	19	1.2	2.23144	2	AC127567	AC127567 Mus muscu
C 570	19	1.2	1.85141	2	AC121913	Mus muscu	C 643	19	1.2	2.23326	2	AC027654	AC027654 Mus muscu
C 571	19	1.2	1.85370	2	AP005066	Oryza sat	C 644	19	1.2	2.23644	10	AL807764	AL807764 Mus muscu
C 572	19	1.2	1.85534	2	AC026620	Homo sapi	C 645	19	1.2	2.29354	2	AC073686	AC073686 Mus muscu
C 573	19	1.2	1.85857	10	AC074311	Mus muscu	C 646	19	1.2	2.29354	14	HEHGMVC	HEHGMVC Homo sapi
C 574	19	1.2	1.85931	9	AC091633	Homo sapi	C 647	19	1.2	2.31463	9	AC094695	AC094695 Rattus no
C 575	19	1.2	1.85957	9	AP000911	Homo sapi	C 648	19	1.2	2.35738	2	AC121365	AC121365 Oryza sat
C 576	19	1.2	1.86014	2	AC111502	Rattus no	C 649	19	1.2	2.36685	2	AC084744	AC084744 Mus muscu
C 577	19	1.2	1.86127	9	AC104582	Homo sapi							

C 650	1.2	241424	9	AC025809	Homo sapi	C 723	18	1.1	1546	10	AF035962	AF035962 Mus muscu
C 651	1.2	246237	3	CEY39B6A	Al132948 Caenorhab	724	18	1.1	1640	6	ARI153502	ARI153502 Sequence
C 652	1.2	247462	3	LMFLCHR.B	AL139794 Leishmani	725	18	1.1	1640	6	I36926	I36926 Sequence 11
C 653	1.2	253050	1	AP000984	AP000984 Sulfolobu	726	18	1.1	1657	9	BC013098	BC013098 Homo sapi
C 654	1.2	253447	2	AL732490	AL732490 Mus muscu	C 727	18	1.1	1658	9	AF359380	AF359380 Homo sapi
C 655	1.2	256989	2	AC123957	AC123957 Mus muscu	728	18	1.1	1667	6	AX250017	AX250017 Sequence
C 656	1.2	266564	2	AC091428	AC091428 Mus muscu	729	18	1.1	1671	10	AF358134	AF358134 Mus muscu
C 657	1.2	302915	3	AE003472	AE003472 Drosophi1	730	18	1.1	1673	8	AY091028	AY091028 Arabidops
C 658	1.2	303191	3	AE003347	AE003347 Drosophi1	731	18	1.1	1678	6	BC003408	BC003408 Homo sapi
C 659	1.2	303760	3	AE003509	AE003509 Drosophi1	C 732	18	1.1	1691	6	AX250019	AX250019 Sequence
C 660	1.2	340000	2	HS21C102	AL163302 Homo sapi	733	18	1.1	1709	9	BC000340	BC000340 Homo sapi
C 661	1.2	347572	2	AC107303	AC107303 Homo sapi	734	18	1.1	1710	9	BC017389	BC017389 Homo sapi
C 662	1.1	18	6	A89478	A89478 Sequence 16	735	18	1.1	1715	9	BC016803	BC016803 Homo sapi
C 663	1.1	18	6	A89487	A89487 Sequence 16	C 736	18	1.1	1733	9	HSAA20513	HSAA20513 Homo sapi
C 664	1.1	18	6	A89488	A89488 Sequence 16	737	18	1.1	1753	9	BC005963	BC005963 Homo sapi
C 665	1.1	18	6	A89489	A89489 Sequence 16	C 738	18	1.1	1756	1	SATGCATA	SA000472 Steaphyloc
C 666	1.1	18	6	A89498	A89498 Sequence 16	C 739	18	1.1	1758	1	SAMWRCATA	AJ000471 Steaphyloc
C 667	1.1	18	6	A89499	A89499 Sequence 16	740	18	1.1	1765	10	BC034838	BC034838 Mus muscu
C 668	1.1	18	20	AR212090	AR212090 Sequence	741	18	1.1	1768	9	AK091884	AK091884 Homo sapi
C 669	1.1	24	6	AX268967	AX268967 Sequence	742	18	1.1	1794	5	GSMART	X83676 Gallus sp.
C 670	1.1	39	6	ARI51068	ARI51068 Sequence	C 743	18	1.1	1829	5	HSU28250	U28250 Human novel
C 671	1.1	39	6	E15024	E15024 PCR primer	744	18	1.1	1848	6	I73512	I73512 Sequence 15
C 672	1.1	96	6	I73509	I73509 Sequence 12	745	18	1.1	1848	12	U06943	U06943 Synthetic C
C 673	1.1	227	8	AY023493	AY023493 Oryza sat	C 746	18	1.1	1892	10	MUSCRGA	M64278 Mouse chrom
C 674	1.1	230	11	G15221	G15221 human STS S	C 747	18	1.1	1907	14	AF076921	AF076921 Chlorella
C 675	1.1	271	9	HSDDT3	AE012434 Homo sapi	C 748	18	1.1	2011	10	MUSAPBPA	M96151 Mus musculu
C 676	1.1	347	11	G06837	G06837 human STS W	C 749	18	1.1	2156	9	BC003193	BC003193 Homo sapi
C 677	1.1	396	4	AF286881	AF286881 Canis fam	C 750	18	1.1	2201	6	AK094124	AK094124 Homo sapi
C 678	1.1	409	6	A68018	A68018 Sequence 13	751	18	1.1	2214	6	AK093957	AK093957 Sequence
C 679	1.1	409	6	ARI63118	ARI63118 Sequence	752	18	1.1	2214	9	E15639	E15639 Pinctada fu
C 680	1.1	415	6	A68020	A68020 Sequence 15	753	18	1.1	2278	9	AK055848	AK055848 Homo sapi
C 681	1.1	415	6	ARI63120	ARI63120 Sequence	754	18	1.1	2306	1	MMAE001959	AF001959 Magneosp
C 682	1.1	430	11	HS242H13T	AL035183 H.sapiens	755	18	1.1	2419	6	ARI64813	ARI64813 Sequence
C 683	1.1	452	3	AY013333	AY013333 Drosophi1	756	18	1.1	2553	9	AK096006	AK096006 Homo sapi
C 684	1.1	465	6	A30539	A30539 R.norvegicu	C 757	18	1.1	2620	9	AK001637	AK001637 Homo sapi
C 685	1.1	480	6	AX276301	AX276301 Sequence	C 758	18	1.1	2842	10	MMU72521	U72521 Mus musculu
C 686	1.1	551	6	AX387786	AX387786 Sequence	C 759	18	1.1	2854	10	MMU72522	U72522 Mus musculu
C 687	1.1	568	6	HSU84143	HSU84143 Homo sapi	C 760	18	1.1	2886	9	AF332199	AF332199 Homo sapi
C 688	1.1	568	9	HSNTCH05	AF058885 Homo sapi	C 761	18	1.1	2899	10	MMU72523	U72523 Mus musculu
C 689	1.1	591	9	BC005971	BC005971 Homo sapi	C 762	18	1.1	2907	10	MDMNOX40	X85214 M.musculu
C 690	1.1	608	9	BC015508	BC015508 Homo sapi	763	18	1.1	2925	9	AK055157	AK055157 Homo sapi
C 691	1.1	666	6	AX410729	AX410729 Sequence	764	18	1.1	2949	3	TBR271083	AJ271083 Trypanoso
C 692	1.1	666	6	HSU49785	UA9785 Human D-dop	765	18	1.1	3038	10	AF181829	AF181829 Mus muscu
C 693	1.1	695	3	TEHHIS2A2A	LI18893 Tetrahymena	C 766	18	1.1	3064	9	HSMB02694	AL359590 Homo sapi
C 694	1.1	735	6	AX331914	AX331914 Sequence	C 767	18	1.1	3172	8	ANGSLKA	X99626 A.niger glik
C 695	1.1	735	6	S74445	S74445 cellular re	C 768	18	1.1	3180	9	AK055202	AK055202 Homo sapi
C 696	1.1	739	9	BC000501	BC000501 Homo sapi	C 769	18	1.1	3295	2	AC084372	AC084372 Homo sapi
C 697	1.1	757	9	BC022069	BC022069 Homo sapi	C 770	18	1.1	3318	6	AX250079	AX250079 Sequence
C 698	1.1	818	5	AF328498	AF328498 Homo sapi	771	18	1.1	3331	3	D86074	D86074 Pinctada fu
C 699	1.1	842	5	AF040525	AF040525 Roeboides	772	18	1.1	3331	6	AR093958	AR093958 Sequence
C 700	1.1	873	6	A72447	A72447 Sequence 34	773	18	1.1	3331	6	AR093959	AR093959 Sequence
C 701	1.1	873	6	A80157	A80157 Sequence 34	774	18	1.1	3331	6	E15640	E15640 Pinctada fu
C 702	1.1	883	10	MMOX40	221674 M.musculu	775	18	1.1	3345	9	AF178985	AF178985 Homo sapi
C 703	1.1	926	6	ARI94569	ARI94569 Sequence	776	18	1.1	3442	9	AK096928	AK096928 Homo sapi
C 704	1.1	1017	10	RSOX40	X17037 Rat mRNA fo	777	18	1.1	3832	9	HSU12535	U12535 Human epide
C 705	1.1	1031	6	ARI64814	ARI64814 Sequence	778	18	1.1	3860	10	AF073294	AF073294 Mus muscu
C 706	1.1	1057	6	HSU09346	U09346 Human urok	779	18	1.1	3892	9	BC030010	BC030010 Homo sapi
C 707	1.1	1113	6	E39390	E39390 Novel Physi	C 780	18	1.1	4030	9	HUMPCAC2A	M97260 Human plasm
C 708	1.1	1133	10	AF079844	AF079844 Rattus no	781	18	1.1	4089	9	AF295024	AF295024 Homo sapi
C 709	1.1	1163	10	AF073798	AF073798 Rattus no	782	18	1.1	4181	6	AX100951	AX100951 Sequence
C 710	1.1	1230	3	CEU72211	U72211 Caenorhabdi	783	18	1.1	4181	6	AX100966	AX100966 Sequence
C 711	1.1	1280	6	ARI68029	ARI68029 Sequence	784	18	1.1	4243	9	BC027711	BC027711 Homo sapi
C 712	1.1	1280	6	AR204800	AR204800 Sequence	785	18	1.1	4260	8	CAU73457	U73457 Candida alb
C 713	1.1	1283	3	AF385333	AF385333 Vanessa c	786	18	1.1	4265	8	AB040904	AB040904 Homo sapi
C 714	1.1	1319	6	AX370170	AX370170 Sequence	C 787	18	1.1	4308	10	MUSNDP1	D10727 Mus musculu
C 715	1.1	1319	10	MUSCHGA	L31361 Mouse chrom	C 788	18	1.1	4421	9	HUMCANP	L00620 Human plasm
C 716	1.1	1370	10	AF020191	AF020191 Mus muscu	789	18	1.1	4456	6	ARI84257	ARI84257 Sequence
C 717	1.1	1401	6	AX172351	AX172351 Sequence	790	18	1.1	4492	6	VSAS1PK	L47210 Candida alb
C 718	1.1	1416	1	AF343352	AF343352 Mus muscu	C 791	18	1.1	4535	9	HSPMCATP	L63575 H.sapiens m
C 719	1.1	1422	1	AB047165	AB047165 Marine CF	C 792	18	1.1	4979	9	HUMATP2B2X	X20977 Human plasm
C 720	1.1	1488	10	BC003702	BC003702 Mus muscu	793	18	1.1	5234	6	BD011689	BD011689 Novel tyr
C 721	1.1	1522	10	AF303745	AF303745 Mus muscu	794	18	1.1	5234	9	AB025194	AB025194 Homo sapi
C 722	1.1	1539	10	AB028854	AB028854 Mus muscu	795	18	1.1	5234	23	BD004111	Bd004111 Novel tyr

DB 847 AATTAGAAAAAGAGATAGACTCTGGCGAGCAAGACCTCAGCCAGCGTCTGTGCCAC 906
QY 507 AAGATGGCAGACATCCGCTGCAGCCGAGACCGCTACTATAGTTCACTGTGGAGCGAC 966
DB 507 AAGGATGCCAGATTCGGCGTGCAGGCCGAGACCGCTACTATAGTTCACTGTGGAGCGAC 966
QY 567 TGGCATCTGTGTC 980
DB 567 TGGCATCTGTGTC 980

RESULT 2
E15017 590 bp DNA linear PAT 28-JUL-1995
LOCUS Canine mRNA for Interleukin 12 40kda subunit, complete cds.
DEFINITION E15017
ACCESSION E15017
VERSION E15017.1 GI:5705700
KEYWORDS JP 1998036397-A/1.
SOURCE
ORGANISM Canis sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 990)
AUTHORS Okano, F.
TITLE CANINE INTERLEUKIN 12 AND ITS PROMOTION
JOURNAL Patent: JP 1998036397-A 1 10-FEB-1998;
TOKAY IND INC

COMMENT OS Canis sp. (dog)
PN JP 1998036397-A/1
PD 10-FEB-1998
PR 08-NOV-1995 JP 1996296789
PK 08-NOV-1995 JP 55P 289725, 23-MAY-1995 JP 56P 128104 P1
OKANO FUMIYOSHI
PC C07K14/54, C07H21/04, C12N5/10, C12N15/09, C12P21/02, (C12N5/10, PC
C12R1:91),
PC (C12P21/02, C12R1:91);
CC strandedness: double;
CC topology: linear;
FH key Location/Qualifiers
FT source 1..590
FT /organism='Canis sp.'
FT /lisse_type='linear'
FT CDS 1..590
FT /product='interleukin 12 40kda subunit',
FEATURES
Location/Qualifiers
L..990
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/db_xref='taxon:9616'
ASE COUNT 27% a 244 c 245 g 218 t
ORIGIN

Query Match 50.9%; Score 974; Db 6; Length 990;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 974; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 247 CGAGATGCTGGCCAGATATACCTGGCCATAAGGAGGCGACGGTCTGAGCCGCTACCTCG 306
QY 307 TTGATTCACAAAAAGAGATGGAATTTGGTCCACTGATATCTTAAAGGACGAAAGAA 366
DB 307 TTGATTCACAAAAAGAGATGGAATTTGGTCCACTGATATCTTAAAGGACGAAAGAA 366
QY 367 TCCAAAAATACATCTTCTGAAATGTGAGGCAAAATATATTCGTGACCTTTTCATATGC 426
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QY 907 AAGGATGCCAAGATCCGCTGCAGGCCGAGACCGCTACTATAGTTCACTGTGGAGCGAC 966
DB 907 AAGGATGCCAAGATCCGCTGCAGGCCGAGACCGCTACTATAGTTCACTGTGGAGCGAC 966
QY 967 TGGCATCTGTGTC 980
DB 967 TGGCATCTGTGTC 980

RESULT 3
CFU49100 1015 bp mRNA linear MAM 13-MAR-1996
LOCUS Canis familiaris interleukin-12 p40 subunit mRNA, complete cds.
DEFINITION U49100
ACCESSION U49100
VERSION U49100.1 GI:1223907
KEYWORDS
SOURCE
ORGANISM Canis familiaris.
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 1015)
AUTHORS Belke-Louis, G.F. and Buettner, M.
TITLE Cloning and sequence analysis of the p35 and p40 subunits of canine interleukin-12
JOURNAL unpublished
REFERENCE 2 (bases 1 to 1015)
AUTHORS Belke-Louis, G.F.
TITLE Direct Submision
JOURNAL Submitted (13-FEB-1996) Georg F. Belke-Louis, Institute of Med. Microbiology, Veterinaerstr. 13, Muenchen, D-80539, Germany

FEATURES

Source

CDS

Location/Qualifiers
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/db_xref="taxon:9615"
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/protein_id="AA92039.1"
/db_xref="GI:1223908"
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MVLTCRPEDEDITMTSAOSEVILGSKETLTVKEFGDAGQYCHKGKVLSSLL
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GESPDQVTCGAVLSARVYVDNRDYKKTYVEQBSGACSAESLDEIVVDAIHK
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BASE COUNT 285 a 251 c 254 g 225 t
ORIGIN

Query Match 50.9%; Score 814; DB 4; Length 1015;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 914; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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185 CAGCCGACAGACGTGAAGTCCCTAGTCTGGTAAACCTGTGACCATCCACATCAAGAAT 244
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185 CAGCCGACAGACGTGAAGTCCCTAGTCTGGTAAACCTGTGACCATCCACATCAAGAAT 244
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245 TTGGAGATGCTGGCAGATATACCTCCATAAAGAGAGCAAGGTTGTGAGCCGCTACATCC 304
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305 TGTGTATTCACAAAAAAGAGATGGAATTTGGTCCACTGATATCTTAAAGAACGAAGA 364
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365 AATCCAAAAATAGATCTTTCTGAAATGTGAGGCAAGAAATTTCTGAGCTTTCACAT 424
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425 GCTGTGCTGACGCGCAATCAGTACTGATTTGAAATTCAGTCTCAAAAGTACAGAGCT 484
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485 TCTCTGACCCCCCAAGGGGTGACATGTGGAGCAGTACACTTTCACAGAGAGGGTCAAG 544
Db
545 TGGCAACAGGAGATTATTAAGAGTACACAGTGGAGTGTGAGAGGGGCGTCCCTGCCCT 604
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725 TGCAGCTGAAGCCATTTGAAAAATTTCTGGGACGTGGAGAGTACGCTGGGAATACCCGCA 784
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725 TGCAGCTGAAGCCATTTGAAAAATTTCTGGGACGTGGAGAGTACGCTGGGAATACCCGCA 784
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785 CCTGAGACACCCCATTTCTTCTCTGACATTTTGGATACAGGCGCCAGGCAAGA 844
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845 ACAATAGAGAAAAAGATAGACTCTGCGTGGACAGACCTCAGCCAAAGTCTGTGCC 904
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965 ACTGGCATCTGTGTC 980
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965 ACTGGCATCTGTGTC 980
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RESULT 4
AR151061
LOCUS
DEFINITION Sequence 1 from patent US 6231850.
ACCESSION AR151061
VERSION AR151061.1 GI:15117111
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 990)
AUTHORS
Okano, F., Satoh, M. and Yamada, K.
TITLE
Canine Interleukin 12
JOURNAL
Patent: US 6231850-A 1 15-MAY-2001;
FEATURES
Source
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/organism="unknown"
BASE COUNT 278 a 243 c 251 g 218 t
ORIGIN

Query Match 49.9%; Score 798; DB 6; Length 990;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 948; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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88 GTTATGTTGTAGAGTTTGACTGGCACCCTGATGCCCCGGAGAAATGTGCTCTCAC 147
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268 TGGCATTAAGAGAGCAGGTTCTGAGCCGCTCACTCTGTTGATTCACAAAAAAGAGAT 327
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328 GGAATTTGGTCCACCTGATATCTTAAGGACAGAAAGATCCAAAAATTAAGATCTTTCTG 387
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388 AAATGTAGAGCAAGAAATTAATTCGACGTTTCAATTCCTGGTGGCTGACGGCAATCAGT 447
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508 TGTGAGCAGAGTACACTTTCAGCAGAGAGGTGAGAGTGTGACATCAGAGGATTTAAGAG 567
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QY 568 TACACAGTGGAGTGTTCAGAGAGGAGTGGCTGGCCCTCTGTCGAGAGAGAGCTTACCACATG 627
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Db 568 TACACAGTGGAGTGTTCAGAGAGGAGTGGCTGGCCCTCTGTCGAGAGAGAGCTTACCACATG 627
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Db 628 GAGGTGCTGGTGGATGCTATTTCACAGGCTCAAGTATGAAACTACAGCAGCAGCTTTCTTC 687
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Db 808 TTCTGCTGACATTTTGATACAGCGCCAGCGCAAGCAAGTATGAGAAAGAAAGATAGAG 867
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Db 868 CTCTGCTGGAGACAGAGCTCAGGCAAGGTGCTGTGTCACAGAGATGCCAAGATTCGCGCTG 927
QY 928 CAAGCCGAGAGCCCTACTATAGTTCATCTGAGCGAGCTGGCGATCTGTG 978
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Db 928 CAAGCCGAGAGCCCTACTATAGTTCATCTGAGCGAGCTGGCGATCTGTG 978

RESULT 5
AF349536 588 bp mRNA Linear MAN 17-MAY-2001
LOCUS
DEFINITION Canis familiaris interleukin-12 subunit p40 mRNA, partial cds.
ACCESSION AF349536
VERSION AF349536.1 GI:14133584
KEYWORDS
SOURCE
ORGANISM
Canis familiaris.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Plissipedia; Canidae; Canis.
REFERENCE
AUTHORS Fontana, S., Groene, A., Koenig, M. and Baumgaertner, W.
TITLE Sequence of canine interleukin-12 p40 mRNA in DH82-cells
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 588)
AUTHORS Fontana, S., Groene, A., Koenig, M. and Baumgaertner, W.
TITLE Direct Submission
JOURNAL Submitted (15-FEB-2001) Institute of Pathology,
Justus-Liebig-University, Frankfurt Str. 56, Giessen 35392,
Germany
FEATURES
Source location/Qualifiers
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/db_xref="taxon:9615"
/cell_line="DH82"
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1..>588
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/protein_id="AAK54070.1"
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/translation="QOLVLSWFSVLILASPLMILELNDYVVEILMHPDAGEWV
LTCITPEPDITDTSQSSSVISGSKITLLOVREPGAGCTGCKKCKVLSRLILH
KKEGIMSTDLIKOKESKNKIFLKEAKNTSGRTFWLTLAISTDLKFSVSSRGS
DPGCVTCGATLTAERVVDNRDKRTYVECEDS"
BASE COUNT 167 a 124 c 155 g 142 t
ORIGIN
Query Match 36.3%; Score 580; DB 4; Length 588;
Best Local Similarity 100.0%; Pred. No. 3; Be-303;
Matches 580; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 CTCACAGTGGTGCATCTGCTGTTTCCGTCGTTTGGTGGCGTCTGCCATGAGCA 60
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Db 61 TATGGGAACTGGAGAGAAAGATGTTATGTTGTAAGCTGGAGCTGGAGCTGATGCCCGG 120
QY 128 GGAATAGTGGTGGCTGCACCTGGCCATACCCCTGAAGAAGATGACATTCAGTGGAGCTAG 187
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Db 121 GGAATAGTGGTGGCTGCACCTGGCCATACCCCTGAAGAAGATGACATTCAGTGGAGCTAG 180
QY 188 CCGACAGCAGTGAAGTCTGAGTTCTGTTAAACCTGTGACATCCACATCAAGTCAAAAGATTGG 247
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Db 181 CCGACAGCAGTGAAGTCTGAGTTCTGTTAAACCTGTGACATCCACATCAAGTCAAAAGATTGG 240
QY 248 GAGATGCTGGCCAGATATACCTGCCATTAAGAGGCAAGGTTCTGAGCCCTGACTCTGT 307
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Db 241 GAGATGCTGGCCAGATATACCTGCCATTAAGAGGCAAGGTTCTGAGCCCTGACTCTGT 300
QY 308 TGATTTCACAAAAGAGAGATGGAATTTGGTCCAGTGATATCTTAAGGACAGAAAGAAAT 367
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Db 301 TGATTTCACAAAAGAGAGATGGAATTTGGTCCAGTGATATCTTAAGGACAGAAAGAAAT 360
QY 368 CCAAAATTAAGATCTTTCTGAAATGTGAGGCAAGAATATTCTGAGCTTTACATGCT 427
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Db 361 CCAAAATTAAGATCTTTCTGAAATGTGAGGCAAGAATATTCTGAGCTTTACATGCT 420
QY 428 GGTGGCTGAGGGCAATCTAGTACTGATTTGAAATTCAGTGTCAAAAGTACAGAGCTTCT 487
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Db 421 GGTGGCTGAGGGCAATCTAGTACTGATTTGAAATTCAGTGTCAAAAGTACAGAGCTTCT 480
QY 488 CTGACCCCGAAGGGGTGATGTGAGCAGTGTGACACTTTACAGCAGAGGGTCAGAGTGG 547
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Db 481 CTGACCCCGAAGGGGTGATGTGAGCAGTGTGACACTTTACAGCAGAGGGTCAGAGTGG 540
QY 548 ACACAGAGGATTTAAGAAGTACACAGTGGAGTGTGAGA 587
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Db 541 ACACAGAGGATTTAAGAAGTACACAGTGGAGTGTGAGA 580

RESULT 6
AR151072 669 bp DNA Linear PAT 08-AUG-2001
LOCUS
DEFINITION Sequence 12 from patent US 6231850.
ACCESSION AR151072
VERSION AR151072.1 GI:15117122
KEYWORDS
SOURCE
ORGANISM
Unknown.
REFERENCE
AUTHORS 1 (bases 1 to 669)
Okano, F., Satoh, M. and Yamada, K.
TITLE Canine Interleukin 12
JOURNAL Patent: US 6231850-A 12 15-MAY-2001;
FEATURES
Source location/Qualifiers
1..669
/organism="unknown"
BASE COUNT 185 a 177 c 144 g 163 t
ORIGIN
Query Match 30.9%; Score 494; DB 6; Length 669;
Best Local Similarity 100.0%; Pred. No. 1; Be-256;
Matches 494; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1076 TGAGAGCCGCTGAGCAACAGCTTCAGAAAGCCGACCAAACTGTAGAAATTATATTCCTGCA 1135
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Db 143 TGAGAGCCGCTGAGCAACAGCTTCAGAAAGCCGACCAAACTGTAGAAATTATATTCCTGCA 202
QY 1136 CTTCCGCAAGAGTTGATCATGTAAGATATACCAAGAGATTAACACGACGACGTGGAGGCT 1195
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Db 203 CTTCCGCAAGAGTTGATCATGTAAGATATACCAAGAGATTAACACGACGACGTGGAGGCT 262
QY 1196 CTTACCACTGGAATTACCATGATGAGAGATTGGCTGGCTTCAGAGAGATCTCTTGA 1255

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Db 263 GCTTACACACTGGAATTAAACATGAGTGTGCTGGCTCCAGAGATCTCTTTGA 322
OY 1256 TTAACAAAGGAGTTGCTGGCTCTGTGAAGGCCCTTTTATGACGGTCCGTCCTTA 1315
Db 323 TAACTAACGGGAGTTGCTGGCTCTGTGAAGGCCCTTTTATGACGGTCTCTGCTTA 382
OY 1316 GCACATCTATGAGACTTGAAGATGTACAGATGGAATTCAGGCCATGAAGCAAGC 1375
Db 383 GCACATCTATGAGACTTGAAGATGTACAGATGGAATTCAGGCCATGAAGCAAGC 442
OY 1376 TTTTAAATGATCCCAAGAGGAGATCTTTCTGATCAAAACATGCTGACACTATCGATG 1435
Db 443 TTTTAAATGATCCCAAGAGGAGATCTTTCTGATCAAAACATGCTGACACTATCGATG 502
OY 1436 AGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCAGAAATCTCCCTTGAAG 1495
Db 503 AGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCAGAAATCTCCCTTGAAG 562
1496 AGCCGATTTTATATAAACTAAATCAAGCTGTGCATCTCTTCATGCTTTGAGAAATTC 1555
563 AGCCGATTTTATATAAACTAAATCAAGCTGTGCATCTCTTCATGCTTTGAGAAATTC 622
OY 1556 GTGCGGTGACCATC 1569
Db 623 GTGCGGTGACCATC 636

RESULT 7
E15018 669 bp DNA linear PAT 28-JUL-1999
LOCUS Canine mRNA for Interleukin 12 35kDa subunit, complete cds.
DEFINITION E15018
ACCESSION E15018.1 GI:5709701
VERSION JP 1998036397-A/2.
KEYWORDS Canis sp.
SOURCE Canis sp.
ORGANISM Canis sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 669)
AUTHORS Okano, F.
TITLE CANINE INTERLEUKIN 12 AND ITS PRODUCTION
JOURNAL Patent: JP 1998036397-A 2 10-FEB-1998;
TORAY IND INC
COMMENT OS Canis sp. (dog)
PN JP 1998036397-A/2
PD 10-FEB-1998
PE 08-NOV-1996 JP 1996296789
PR 08-NOV-1995 JP 95P 289729, 23-MAY-1996 JP 96P 128104 PI
OKANO FUMIYOSHI
PC C07K14/54, C07H21/04, C12N5/10, C12N15/09, C12P21/02, C12N5/10, PC
C12R1:91),
PC (C12P21/02, C12R1:91):
CC strandedness: Double;
CC topology: Linear;
FH Key Location/Qualifiers
FH source 1..669
FT /organism="Canis sp."
FT /tissue_type="liver"
FT CDS 1..669
FT /product="interleukin12 35kDa subunit".
FEATURES
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1..669
Location/Qualifiers
1..669
/organism="Canis sp."
/db_xref="taxon:9616"
BASE COUNT 185 a 177 c 144 g 163 t
ORIGIN
Query Match 30.9%; Score 494; DB 6; Length 669;
Best Local Similarity 100.0%; Pred. No. 1,8e-256;
Matches 494; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1076 TGAGAGCCGTGACGACAGCGCTTGAGAGGCCAGACAAACTCTAGAAATATATTCCTGCA 1135
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OY 1136 CTTCCGAAGACATTTGATCATAGATATACAAAGAGATAAACCAGCAGCAGTGGAGGCT 1195
Db 203 CTTCCGAAGACATTTGATCATAGATATACAAAGAGATAAACCAGCAGCAGTGGAGGCT 262
OY 1196 GCTTACACACTGGAATTAAACATGAGTGTGCTGGCTCCAGAGATCTCTTTGA 1255
Db 263 GCTTACACACTGGAATTAAACATGAGTGTGCTGGCTCCAGAGAGATCTCTTTGA 322
OY 1256 TTAACAAAGGAGTTGCTGGCTCTGTGAAGGCCCTTTTATGACGGTCTCTGCTTA 1315
Db 323 TTAACAAAGGAGTTGCTGGCTCTGTGAAGGCCCTTTTATGACGGTCTCTGCTTA 382
OY 1316 GCACATCTATGAGACTTGAAGATGTACAGATGGAATTCAGGCCATGAAGCAAGC 1375
Db 383 GCACATCTATGAGACTTGAAGATGTACAGATGGAATTCAGGCCATGAAGCAAGC 442
OY 1376 TTTTAAATGATCCCAAGAGGAGATCTTTCTGATCAAAACATGCTGACACTATCGATG 1435
Db 443 TTTTAAATGATCCCAAGAGGAGATCTTTCTGATCAAAACATGCTGACACTATCGATG 502
OY 1436 AGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCAGAAATCTCCCTTGAAG 1495
Db 503 AGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCAGAAATCTCCCTTGAAG 562
OY 1496 AGCCGATTTTATATAAACTAAATCAAGCTGTGCATCTCTTCATGCTTTGAGAAATTC 1555
Db 563 AGCCGATTTTATATAAACTAAATCAAGCTGTGCATCTCTTCATGCTTTGAGAAATTC 622
OY 1556 GTGCGGTGACCATC 1569
Db 623 GTGCGGTGACCATC 636

RESULT 8
AF333121 452 bp mRNA linear MAM 06-FEB-2001
LOCUS Canis familiaris Interleukin 12 subunit p40 mRNA, partial cds.
DEFINITION AF333121
ACCESSION AF333121
VERSION AF333121.1 GI:12667429
KEYWORDS Canis familiaris.
SOURCE Canis familiaris.
ORGANISM Canis familiaris.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 452)
AUTHORS Markus, S. and Baumgaertner, W.
TITLE Expression of canine interleukin-12 subunit p40 mRNA in a
continuous macrophage cell line
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 452)
AUTHORS Markus, S. and Baumgaertner, W.
TITLE Direct Submission
JOURNAL Submitted (03-JAN-2001) Department of Veterinary Pathology,
Justus-Liebig-University of Giessen, Frankfurt Strasse 96,
Giessen 35392, Germany
FEATURES
source
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Location/Qualifiers
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/organism="Canis familiaris"
/db_xref="taxon:9615"
/cell_line="DH 82"
/cell_type="macrophage"
/feature="amplified using primer pair p77s/p34as"
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/product="interleukin 12 subunit p40"
/protein_id="AAK01441.1"
/db_xref="GI:12667430"
/translation="TCHPPEEDDITWTSQSSSEVLGSGKTLTIQVKEFPDAGQYCHK
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BLKFSVRSKRCHSPDQGVYTCGAVTHSAERVVDVNDKRYVECEQGS"
BASE COUNT 144 a 90 c 117 g 101 t
ORIGIN
Query Match 27.8% Score 444: DB 4: Length 452:
Best Local Similarity 100.0%: Pred. No. 2.7e-229:
Matches 444: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
QY 144 CACCTGCCATFAGCCGTGAAGACATGACATCACTTGACCTCGCCAGCGACAGCTAGCT 203
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DB 1 CACCTGCCATFAGCCGTGAAGACATGACATCACTTGACCTCGCCAGCGACAGCTAGCT 60
QY 204 CCTAGGCTTCTGTAAACCTCTGACCATCCAGTCGAAAGATTTGGAGATCTTGCCAGTA 263
|||||
DB 61 CCTAGGCTTCTGTAAACCTCTGACCATCCAGTCGAAAGATTTGGAGATCTTGCCAGTA 120
QY 264 TACCTGCGATTAAGAGAGGCAAGGTTCTGAGCGCCCTCATCTCTTGATTCACAAAAAGA 323
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DB 121 TACCTGCGATTAAGAGAGGCAAGGTTCTGAGCGCCCTCATCTCTTGATTCACAAAAAGA 180
Y 324 AGATGCAATTTGGTCACATATCTTAAAGGAGAGAAAGATCCGAAAATTAAGATCTT 383
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DB 181 AGATGCAATTTGGTCACATATCTTAAAGGAGAGAAAGATCCGAAAATTAAGATCTT 240
QY 384 TCTGAATGTGAGGCAAGATTAATCTGACGCTTTGACATGCTGGTGCTGACGGCAAT 443
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DB 241 TCTGAATGTGAGGCAAGATTAATCTGACGCTTTGACATGCTGGTGCTGACGGCAAT 300
QY 444 CACTACTGATTTGAATTAATTAAGTACAGAGGCTTCTTGACGCCCAAGGGGT 503
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DB 301 CACTACTGATTTGAATTAATTAAGTACAGAGGCTTCTTGACGCCCAAGGGGT 360
QY 504 GACATCTGAGGCGGTCAGACTTTGACGAGGAGGCTTACGTCGACACAGCGGATATAA 563
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DB 361 GACATCTGAGGCGGTCAGACTTTGACGAGGAGGCTTACGTCGACACAGCGGATATAA 420
QY 564 GAAGTACACAGCTGAGCTGCAGGA 587
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DB 421 GAAGTACACAGCTGAGCTGCAGGA 444
RESULT 9
ARI51062 669 bp DNA linear PAT 08-AUG-2001
LOCUS
DEFINITION Sequence 2 from patent US 6231850.
ACCESSION ARI51062
VERSION ARI51062.1 GI:15117112
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 669)
AUTHORS Okano, F., Satoh, M. and Yamada, K.
TITLE Canine Interleukin 12
JOURNAL Patent: US 6231850-A 2 15-MAY-2001:
FEATURES
source 1..669
location/Qualifiers
BASE COUNT 183 a 178 c 146 g 162 t
ORIGIN
Query Match 27.7% Score 443: DB 6: Length 669:
Best Local Similarity 99.8%: Pred. No. 9.4e-229:
Matches 493: Conservative 0: Mismatches 1: Indels 0: Gaps 0:
QY 1076 TAGAGGCTCTCAGCAACACCTTCAGAGAGCCAGACAACTCTAGAATTAATTTCTGCA 1135
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DB 143 TAGAGGCTCTCAGCAACACCTTCAGAGAGCCAGACAACTCTAGAATTAATTTCTGCA 202
QY 1136 CTTCCGAAGAGATTGATCATGAAGATATCGCAAGGATAAACCAGCAGCTGGAGGCTT 1195
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DB 203 CTTCCGAAGAGATTGATCATGAAGATATCGCAAGGATAAACCAGCAGCTGGAGGCTT 262

QY 1196 GCTTACCAGTGGGAATTAAACCATGATGAGAGTTGGCTGGCTTCAGAGAGATCTTTGA 1255
|||||
DB 263 GCTTACCAGTGGGAATTAAACCATGATGAGAGTTGGCTGGCTTCAGAGAGATCTTTGA 322
QY 1256 TAACTAAGCGGAGTGGCTGGCTTCGAAAGGCTCTTTTATGACGGTCTTGCCCTTA 1315
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DB 323 TAACTAAGCGGAGTGGCTGGCTTCGAAAGGCTCTTTTATGACGGTCTTGCCCTTA 382
QY 1316 GCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCGAAGGCCATGAACGCAAGC 1375
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DB 383 GCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCGAAGGCCATGAACGCAAGC 442
QY 1376 TTTTAAATGATCCCAAGAGGACAGATCTTTCTGATGATGAAAACATGTCGACAGCTATGATG 1435
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DB 443 TTTTAAATGATCCCAAGAGGACAGATCTTTCTGATGATGAAAACATGTCGACAGCTATGATG 502
QY 1436 AGCTGTTACAGGCGCTGGAATTTTCAGAGTGTGACTGTGCCAGAAATCCCTCTGGAAG 1495
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DB 503 AGCTGTTACAGGCGCTGGAATTTTCAGAGTGTGACTGTGCCAGAAATCCCTCTGGAAG 562
QY 1496 AGCCGATTTTAAACTAAATACAGCTGTGATCTTTCTTCAATGCTTTGAGAAATTC 1555
|||||
DB 563 AGCCGATTTTAAACTAAATACAGCTGTGATCTTTCTTCAATGCTTTGAGAAATTC 622
QY 1556 GTGCGGTGACCATTC 1569
|||||
DB 623 GTGCGGTGACCATTC 636
RESULT 10
CF049085 669 bp mRNA linear MAN 13-MAR-1996
LOCUS
DEFINITION Canis familiaris Interleukin-12 p35 subunit mRNA, complete cds.
ACCESSION U49085
VERSION U49085.1 GI:1223905
KEYWORDS
SOURCE
ORGANISM
Canis familiaris.
Canis familiaris.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 669)
AUTHORS Belke-Louis, G.F. and Bueltner, M.
TITLE Cloning and sequence analysis of the p35 and p40 subunits of canine
Interleukin-12
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 669)
AUTHORS Belke-Louis, G.F.
TITLE Direct Submission
JOURNAL Submitted (13-FEB-1996) Georg F. Belke-Louis, Institute of Med.
Microbiology, Veterinaerstr. 13, Muenchen, D-80539, Germany
FEATURES
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location/Qualifiers
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/db_xref="taxon:9615"
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/protein_id="AA92058.1"
/db_xref="GI:1223905"
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ONLRVSNITOKAROLDYIPCTSEEDIHEDITDKSTVACPLDELTMNSCLAS
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NMLTALDELQALNNSVTVPOKSSLEEDPFYKIKILCLILHAFIRAVYIDRMKST
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BASE COUNT 183 a 177 c 145 g 164 t
ORIGIN
Query Match 24.3% Score 389: DB 4: Length 669:
Best Local Similarity 99.8%: Pred. No. 2.1e-199:
Matches 439: Conservative 0: Mismatches 1: Indels 0: Gaps 0:
QY 1130 CTTGCATCTCCGAGAGATTGATCATGAGATATCAAAAGATTAAGCAGCAGCTGG 1189
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Db	197	CGCGACCTTCCGAACAGATTGATCATGAAGAATATCAACAAGAGATTAAACACACACAGTGG	256
QY	1190	AGGCTGCTTTACCACTGCAATTAACCATGAATGAGAGTTGGCTGCTTCACAGAGATCT	1249
Db	257	AGGCTGCTTACCACTGGAATTAACCATGAATGAAGAAGTGGCTGCTTCACAGAGATCT	316
QY	1250	CTTTGATTAACATAAGGGAGTTGGCTGGGCTCTGGAAAGGCCCTTTTATGACAGTCCT	1309
Db	317	CTTTGATTAACATAAGGGAGTTGGCTGGGCTCTGGAAAGGCCCTTTTATGACAGTCCT	376
QY	1310	GCCTTACGACGATCTATAGACCTTGAAGATGTACACAGTGAATTTCAAGCCATGAAC	1369
Db	377	GCCTTACGACGATCTATAGAGACTTGAAGATGTACACAGTGAATTTCAAGCCATGAAC	436
QY	1370	CAAACTTTTATGATGCCCAAGAGGCGATCTTTCTGGATCAAAACATGCTGACAGCTA	1429
Db	437	CAAACTTTTATGATGCCCAAGAGGCGATCTTTCTGGATCAAAACATGTTGACAGCTA	496
QY	1430	TGCGATGACCTGTATAGAGCCCTGAATTTCAACAGTGTAGTGTGGCACAGAAATCTCCG	1489
Db	497	TGCGATGACCTGTATAGAGCCCTGAATTTCAACAGTGTAGTGTGGCACAGAAATCTCCG	556
QY	1490	TTGAAGAGCCGGGATTTTATAAACATAAATCAACCTGTGCTACTTCTCATGCTTTCA	1549
Db	557	TTGAAGAGCCGGGATTTTATAAACATAAATCAACCTGTGCTACTTCTCATGCTTTCA	616
QY	1550	GAATTCGTGGCGGTGACCATC	1569
Db	617	GAATTCGTGGCGGTGACCATC	636

RESULT_11	LOCUS	DEFINITION	ACCESSION	VERSION
AF091134	446 bp	mrna	linear	MAM 04-AUG-1999
		Canis familiaris interleukin-12 p40 mRNA, partial cds.		
AF091134				
AF091134.1	GI:5690205			

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
Mammalia: Eutheria; Carnivora: Flissipedia; Canidae; Canis.
1 (bases 1 to 446)
German, A.J., Helps, C.R., Harley, R., Hall, E.J. and Day, M.J.
Cloning and sequencing of canine IL-12 p40 mRNA
unpublished
2 (bases 1 to 446)
German, A.J., Helps, C.R., Harley, R., Hall, E.J. and Day, M.J.
Direct Submission
Submitted (12-SEP-1998) Department of Clinical Veterinary Science,

FEATURES	Location/Qualifiers
SOURCE	1. .446

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CDS	<1. .>446	

BASE COUNT	ORIGIN
133	a
91	c
120	g
102	t

Query March Similarity	24.2%	Score 387	DB 4	Length 446
Best Local Similarity	99.8%	Pred. No. 2.5e-196		
Matches 437	Conservative 0	Mismatches 1	Indels 0	Gaps 0

212 CTGTAACCTCTGACCATCCAAGTCAAGAATTGGAGATGCTGGCCAGTATACCTGCC 271

Db	8	CTGGTAAACCTGTGACCATCCAAAGTCAAGAAATTTGGAGATGCTGGCCAGTATACCTGCC	67
OY	272	ATAAGGAGGCGAAGGCTTCTGAGCCCTCCTACCTCTTATTCACAAAAAGAAAGTGGAA	331
Db	68	ATAAAGAGGCGCAGGTTCTGAGCCGCTACTCTCTTTGATTCACAAAAAGAAAGTGGAA	127
OY	332	TTTGGTCACCTGATATCTTTAAAGCAACAGAAAGAAATTCAGAAATTAAGTCTTTCTGAAT	391
Db	128	TTTGGTCACCTGATATCTTTAAAGCAACAGAAAGAAATTCAGAAATTAAGTCTTTCTGAAT	187
OY	392	GTGAGGCAAGAATTAATCTGAGCTTTTCACACTGCTGGTGGCTGAGCGCAATCACTACTG	451
Db	188	GTGAGGCAAGAATTAATCTGAGCTTTTCACACTGCTGGTGGCTGAGCGCAATCACTACTG	247
OY	452	ATTTGAATTTGAGTGTCAAAAGTACGACAGAGGCTCTGACCCCCCAAGGGGTGCATCTG	511
Db	248	ATTTGAATTTGAGTGTCAAAAGTACGACAGAGGCTCTCTGACCCCCCAAGGGGTGCATCTG	307
OY	512	GAGCAGTGACACTTTCACACAGAGAGGTTCAGAGTGGACACAGGATTAATAAGAGTACA	571
Db	308	GAGCAGTGACACTTTCACACAGAGAGGTTCAGAGTGGACACAGGATTAATAAGAGTACA	367
OY	572	CAGTGGAGTGTACAGAGGGCAGTGCCTGCCCTCTGCCGAGAGAGCCTACCACATCGAG	631
Db	368	CAGTGGAGTGTACAGAGGGCAGTGCCTGCCCTCTGCCGAGAGAGCCTACCACATCGAG	427
OY	632	TCGTGGTGGATGCTATTTC	649
Db	428	TCGTGGTGGATGCTATTTC	445

RESULT 12	AX154603	AX154603	990 bp	DNA	1 linear	PAT 22-JUN-2001
LOCUS	AX154603					
DEFINITION	Sequence	7 from Patent WO0140257.				
ACCESSION	AX154603					
VERSION	AX154603.1	GI:14536186				

ORGANISM	synthetic construct
REFERENCE	artificial sequences.
AUTHORS	1 (bases 1 to 990)
TITLE	Leon, S.R. and Punnonen, J.
JOURNAL	Cycline polypeptides and nucleic acids
	Patent: WO 0140257-A 7 07-JUN-2001;

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source      location/Qualifiers
FEATURES
1. .990    /organism="synthetic construct"

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BASE COUNT	/mole—synthetic sequence			
ORIGIN	a	c	g	t
	270	250	254	216

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Best Local Similarity	100.0%	Pred. No.	9.9e-66	
Matches 143	Conservative	0	Mismatches	0
			Indels	0
			Gaps	0

QY	565	AAGTACACAGTGGAGTGT	CAGAGAGGCGAGTCCCTG	CGCCGAGGAGAGCCCTACCC	624
Db	565	AAGTACACAGTGGAGTGT <td>CAGAGAGGCGAGTCCCTG <td>CGCCGAGGAGAGCCCTACCC</td> <td>624</td> </td>	CAGAGAGGCGAGTCCCTG <td>CGCCGAGGAGAGCCCTACCC</td> <td>624</td>	CGCCGAGGAGAGCCCTACCC	624
QY	625	ATCGAGGTCTGGTGGATGCTATT <td>CACCAAGTCAAGTTG <td>AAAACTACACCAAGCAGCTTTC</td> <td>684</td> </td>	CACCAAGTCAAGTTG <td>AAAACTACACCAAGCAGCTTTC</td> <td>684</td>	AAAACTACACCAAGCAGCTTTC	684
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Db 685 TTGATCAGAGACATCATCAACC 707

RESULT 1.3


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AX154599
LOCUS AX154599 984 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 3 from Patent WO0140257.
ACCESSION AX154599
VERSION AX154599.1 GI:14536182
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 984)
AUTHORS Leong,S.R. and Punnonen,J.
TITLE Cytokine polypeptides and nucleic acids
JOURNAL Patent: WO 0140257-A 3 07-JUN-2001;
Maxygen, Inc. (US)
FEATURES
Source location/Qualifiers
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/db_xref="taxon:32630"
/note="Synthetic Sequence"

BASE COUNT 267 a 246 c 254 g 217 t
ORIGIN

Query Match 5.9%; Score 95; DB 6; Length 984;
Best Local Similarity 100.0%; Pred. No. 1.4e-57;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 586 GAGGGCAGTGCCTGCTCTCTGCGAGGAGAGCCTACCCATCGAGCTGCTGTGATGCT 645
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DB 586 GAGGGCAGTGCCTGCTCTCTGCGAGGAGAGCCTACCCATCGAGCTGCTGTGATGCT 645
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QY 646 ATTCACAGCTCAGATATGAAAGTACACGACGAG 680
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DB 646 ATTCACAGCTCAGATATGAAAGTACACGACGAG 680
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RESULT 15
AF054605
LOCUS AF054605 285 bp mRNA linear MAM 26-JUL-2000
DEFINITION Felis catus interleukin 12 p35 subunit mRNA, partial cds.
ACCESSION AF054605
VERSION AF054605.1 GI:3126818
KEYWORDS
SOURCE Felis catus.
ORGANISM Felis catus
REFERENCE 1 (bases 1 to 285)
AUTHORS Harley,R., Helps,C.R., Harbour,D.A., Gruffydd-Jones,T.J. and
Day,M.J.
TITLE Cytokine mRNA expression in lesions in cats with chronic
gingivostomatitis
JOURNAL Clin. Diagn. Lab. Immunol. 6 (4), 471-478 (1999)
MEDLINE 99322318
PubMed 10391845
REFERENCE 2 (bases 1 to 285)
AUTHORS Harley,R., Helps,C.R., Gruffydd-Jones,T.J., Day,M.J. and
Harbour,D.A.
TITLE Direct Submission
JOURNAL Submitted (19-MAR-1998) Clinical Veterinary Science, University of
Bristol, Langford House, Langford, Bristol BS40 7DU, U.K.
FEATURES
Source location/Qualifiers
1..285
/organism="Felis catus"
/db_xref="taxon:9685"
/cell_line="Fid"
/cell_type="T cell"
/note="persistent FIV infection"
<1..>285
/codon_start=3
/product="interleukin 12 p35 subunit"
/protein_id="AAC15978.1"
/db_xref="GI:3126819"
/translation="LIRALISNLIHKARQTLFVYSCSTSEIDHEDITKQKTSVEACLP
LEITMNSCLASREISLIYNGSCLASRKTSFMTTLCLSSIEDLKMYYE"

BASE COUNT 84 a 70 c 64 g 67 t
ORIGIN

Query Match 5.1%; Score 81; DB 4; Length 285;
Best Local Similarity 100.0%; Pred. No. 4.7e-32;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1171 GATAAACGACGACAGTGGAGGCTGCTTACCACTGGAATTACCATGATGAGAGTTGC 1230
|||||
DB 102 GATAAACGACGACAGTGGAGGCTGCTTACCACTGGAATTACCATGATGAGAGTTGC 161
|||||

QY 1231 CTGGCTTCGACAGAGATCTCT 1251
|||||
DB 162 CTGGCTTCGACAGAGATCTCT 182
|||||

```

Search completed: January 21, 2003, 16:43:42
 Job time : 2902 secs

GenCore version 5.1.3
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om nucleic - nucleic search, using sw model

Run on: January 21, 2003, 15:00:38 : Search time 245 Seconds
(without alignments)
14697.736 Million cell updates/sec

Title: US-09-917-265-61

Perfect score: 1599

Sequence: 1 atgcacccctggccgcttggct.....tgcctcctctgaacctctcc 1599

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 1125999159 residues

ord size : 0

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: listing first 1000 summaries

Database : N_Geneseq_101002:*

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- 24: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pried. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	974	60.9	990	19	AAV1817
2	974	60.9	990	20	AAV35625
3	974	60.9	990	20	AAV35625
4	974	60.9	990	20	AAV35625
5	974	60.9	990	20	AAV35625
6	974	60.9	990	20	AAV35625
7	974	60.9	990	20	AAV35625
8	974	60.9	990	20	AAV35625
9	974	60.9	990	20	AAV35625

10	658	41.2	2154	20	AAV18176	Canine full length
11	494	30.9	591	20	AAV18179	Canine mature CLAF
12	494	30.9	591	20	AAV18181	Canine IL-12 p35 S
13	494	30.9	591	20	AAV35626	Nucleic acid encod
14	494	30.9	591	20	AAV35626	Nucleic acid encod
15	494	30.9	591	20	AAV35626	Nucleic acid encod
16	494	30.9	591	20	AAV35626	Nucleic acid encod
17	494	30.9	591	20	AAV35626	Nucleic acid encod
18	494	30.9	591	20	AAV35626	Nucleic acid encod
19	494	30.9	591	20	AAV35626	Nucleic acid encod
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23	494	30.9	591	20	AAV35626	Nucleic acid encod
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81	494	30.9	591	20	AAV35626	Nucleic acid encod
82	494	30.9	591	20	AAV35626	Nucleic acid encod

83	59	3.7	8644	24	AAD31551	PIRES-IL12.3-hb7-1	C 156	21	1.3	76	22	AAF26093	Feline IL-12p35 PC
84	59	3.7	8659	24	AAD31550	PIRES-IL12.4-hb7-1	157	21	1.3	76	22	AAF26100	Feline IL-12 assoc
85	56	3.5	6639	22	AAF26098	PIRES PMOL-fil12	C 158	20	1.3	20	17	AAT39015	Interleukin IL-12
86	56	3.5	669	22	AAF26083	Feline IL-12p35 en	C 159	20	1.3	30	22	AA165150	Canine IL12p40 gen
87	56	3.5	669	22	AAF26086	Feline IL-12p35 en	C 160	20	1.3	39	19	AAV13827	Primer for canine
88	56	3.5	683	22	AAF26096	Human pg-hIL12p DN	C 161	20	1.3	39	20	AAV35628	PCR primer for nuc
89	56	3.5	4201	22	AAF26077	Feline IL-12p35 en	C 162	20	1.3	39	20	AAV33165	PCR primer used to
90	46	2.9	906	11	AAO04701	Sequence encoding	C 163	20	1.3	39	22	AA164391	PCR primer #10. U
91	46	2.9	975	22	AAD15208	Cytotoxic lymphocy	164	20	1.3	73	22	AA153322	Mouse IL-12 p40 #1
92	46	2.9	979	12	AAO12149	Modified human cyt	165	20	1.3	600	20	AAV78397	IL-12p40 cDNA frag
93	46	2.9	987	16	AAO97484	Human interleukin-	166	20	1.3	600	20	AAV25947	Interleukin 12 p40
94	46	2.9	987	19	AAV07273	Human interleukin-	C 167	20	1.3	720	20	AAV13783	Human breast cance
95	46	2.9	987	19	AAV07217	DNA encoding human	C 168	20	1.3	790	22	AAV12650	Human breast cance
96	46	2.9	987	20	AAZ40404	Human interleukin	169	20	1.3	1056	19	AAV28472	Murine interleukin
97	46	2.9	987	20	AAV83199	Interleukin (IL)-1	170	20	1.3	1061	17	AAV25200	Murine interleukin-
98	46	2.9	987	22	AAD15210	Human cytokine p40	171	20	1.3	1409	22	AAV68879	Murine p40-GM-CSF
99	46	2.9	1007	22	AAD18585	Human interleukin-	172	20	1.3	1472	22	AAV68879	Murine p40-IL-2 co
100	46	2.9	1018	15	AAO67879	EPV 42 KD promoter	C 173	20	1.3	3152	23	ABL19511	Drosophila melanog
101	46	2.9	1018	20	AAZ08510	EPV 42 KDa/human I	C 174	20	1.3	3425	23	ABL05265	Drosophila melanog
102	46	2.9	1389	22	AAV76880	Human p40-IL-2 cod	C 175	20	1.3	3638	23	ABL18371	Drosophila melanog
103	46	2.9	1397	18	AAV00401	40 kDa subunit of	176	20	1.3	6851	23	ABL19510	Drosophila melanog
104	46	2.9	1397	18	AAV77849	40 kDa subunit of	177	20	1.3	14103	23	ABL18370	Drosophila melanog
105	46	2.9	1397	18	AAV97969	40 kDa subunit of	178	20	1.3	14422	23	ABL05264	Drosophila melanog
106	46	2.9	1397	19	AAV37767	Cytotoxic lymphocy	179	19	1.2	21	22	AAH33353	IL-12/p40 (sense)
107	46	2.9	1399	21	AAZ40021	Human p40 coding s	180	19	1.2	21	22	AAV31346	Murine splenocyte
108	46	2.9	2362	13	AAQ23586	Natural killer cell	181	19	1.2	21	24	AAZ24889	Interleukin-12p40
109	46	2.9	2362	17	AAV48098	Human interleukin-	C 182	19	1.2	25	21	AAZ40018	PCR primer for p40
110	46	2.9	2362	19	AAV42535	Human interleukin-	183	19	1.2	30	21	AAV70706	Bovine interleukin
111	46	2.9	2362	19	AAV15227	Heterodimeric huma	184	19	1.2	30	21	AAV05702	Oligonucleotide SE
112	46	2.9	2362	21	AAZ28862	Human interleukin-	C 185	19	1.2	144	22	AAK83085	Human immune/haema
113	46	2.9	2362	22	AAV56280	IL-12 vaccine adju	C 186	19	1.2	147	23	ABL26545	Drosophila melanog
114	46	2.9	18110	24	ABK15357	Human interleukin	C 187	19	1.2	208	21	AAV12941	Human secreted pro
115	46	2.9	18340	22	AAD19368	Mammalian Interleu	188	19	1.2	489	23	ABL23947	Drosophila melanog
116	44	2.8	984	18	AAV50759	Sequence of ovine	C 189	19	1.2	615	22	AAH98857	Human EST-derived
117	44	2.8	1019	20	AAV70709	Bovine interleukin	190	19	1.2	759	24	ABO91601	M. capsulatus gene
118	43	2.7	79	21	AAV18181	Primer for Canine	C 191	19	1.2	849	22	AAH45857	Porcine Fas ligand
119	43	2.7	660	22	AAD15219	Modified human cyt	C 192	19	1.2	1320	24	ABK15358	Human Interleukin
120	34	2.1	984	22	AAD15204	Modified human cyt	193	19	1.2	1334	23	ABL17353	Drosophila melanog
121	33	2.1	33	17	AAT35197	(Glyc)Ser linker D	194	19	1.2	1461	22	ABA89197	Escherichia coli p
122	31	1.9	582	22	AAV76877	Mature murine p35	195	19	1.2	2092	24	ABO15296	Oligonucleotide fo
123	31	1.9	660	20	AAV78396	IL-12p35 cDNA frag	C 196	19	1.2	2092	24	ABO15297	Human prostate can
124	31	1.9	660	20	AAV25946	Interleukin 12 p35	C 197	19	1.2	2197	21	AAV16032	Human polynucleoti
125	31	1.9	713	17	AAT35199	Mouse interleukin-	C 198	19	1.2	2197	20	ABL90767	Human ELK-1 encodi
126	31	1.9	1265	19	AAV28473	Murine interleukin	C 199	19	1.2	2266	20	AAZ41049	Human ELK-1 nucleo
127	31	1.9	1278	22	AAV76881	DNA encoding fusio	C 200	19	1.2	2266	20	AAZ06608	Drosophila melanog
128	31	1.9	1569	22	AAV76888	Single-chain murin	201	19	1.2	2265	23	ABL26544	Drosophila melanog
129	31	1.9	2013	22	AAV76887	Murine p35-linker-	C 202	19	1.2	2489	23	ABL23946	Drosophila melanog
130	31	1.9	2709	22	AAV76889	Coding sequence of	C 203	19	1.2	2931	23	ABL17352	Drosophila melanog
131	31	1.9	5966	20	AAZ40417	Plasmid pIN0961 co	C 204	19	1.2	3006	24	ABO55079	Human ovarian anti
132	31	1.9	6295	19	AAV02043	Plasmid pWRG3196 e	C 205	19	1.2	3058	22	AAV80597	Receptor #85 part1
133	31	1.9	7287	19	AAV02042	Bovine interleukin	C 206	19	1.2	3127	22	AAV45970	Human cDNA encodin
134	29	1.8	703	21	AAV70708	Reproductive recom	C 207	19	1.2	3163	21	AAV27981	Human netrin-like
135	27	1.7	42	24	AAV44012	Reproductive recom	208	19	1.2	3207	12	AAO14263	p-metA-1 metastasi
136	27	1.7	42	24	AAV44013	Reproductive recom	209	19	1.2	5019	19	AAV34855	Human retinal dege
137	27	1.7	79	19	AAV56639	Feline FLAF cDNA p	210	19	1.2	5200	18	AAV02302	Rat tumor suppres
138	26	1.6	554	18	AAT50757	Partial sequence o	211	19	1.2	6273	23	ABL15731	Drosophila melanog
139	25	1.6	71	22	AAV26092	Feline IL-12p35 PC	C 212	19	1.2	10855	23	ABL15730	Drosophila melanog
140	25	1.6	71	22	AAV26099	Feline IL-12 assoc	C 213	19	1.2	11534	23	ABL03590	Drosophila melanog
141	24	1.5	30	22	AA165149	Canine IL12p40 gen	C 214	19	1.2	14147	22	AAV46744	Tumour suppressor
142	24	1.5	36	20	AAV18182	Primer for Canine	215	19	1.2	14147	22	ABK33956	Human DNA for stag
143	24	1.5	39	19	AAV13826	Primer for Canine	C 216	19	1.2	17294	24	ABL2986	Human immune syste
144	24	1.5	39	20	AAV35627	PCR primer for nuc	C 217	19	1.2	34688	24	ABO67060	Human angiogenesis
145	24	1.5	39	20	AAV03164	PCR primer used to	C 218	19	1.2	48715	22	ABA89188	Escherichia coli p
146	24	1.5	666	18	AAV64390	PCR primer #9. Un	C 219	19	1.2	145831	24	ABL62309	Colon adenocarcino
147	24	1.5	666	18	AAV50758	Sequence of ovine	C 220	19	1.2	145831	24	ABL66806	Lung cancer relate
148	24	1.5	987	20	AAZ40405	Human interleukin	C 221	19	1.2	145831	24	ABL68588	Kidney cancer rela
149	24	1.5	987	20	AAZ40406	Human interleukin	C 222	19	1.2	145831	24	ABL69213	Prostate cancer re
150	23	1.4	200	19	AAV03357	Homo sapiens Inter	C 223	18	1.1	24	22	AAV15293	Mouse IL-12 p40 #1
151	23	1.4	1947	22	AAV25019	Nucleotide sequenc	C 224	18	1.1	39	19	AAV13825	PCR primer for canin
152	21	1.3	30	18	AAV50768	Ovine IL-12 40 KD	C 225	18	1.1	39	20	AAV35622	PCR primer for nuc
153	21	1.3	32	19	AAV26188	bIL-12 p40 gene PC	C 226	18	1.1	39	20	AAV03155	PCR primer used to
154	21	1.3	44	19	AAV56632	Feline FLAF cDNA p	C 227	18	1.1	39	20	AAV64385	PCR primer #6. Un
155	21	1.3	76	22	AAV26090	Feline IL-12p35 PC	C 228	18	1.1	65	24	ABN55508	Mouse spliced tran

229	18	1.1	316	24	ABN205956	Human ORFX polyuuc	302	18	1.1	3094	21	AA593124	Human secreted pro
230	18	1.1	358	21	AAC22538	Human secreted pro	303	18	1.1	3125	23	AA578013	DNA encoding novel
C 231	18	1.1	362	21	AAC03124	Human secreted pro	304	18	1.1	3125	23	AA580668	DNA encoding novel
C 232	18	1.1	409	19	AAV13075	Cellulase activity	305	18	1.1	3230	22	AA580094	Human lung antigen
233	18	1.1	415	19	AAV13077	Cellulase activity	306	18	1.1	3331	19	AAV22683	Human DNA sequence 1
234	18	1.1	416	21	AA433965	Zea mays DNA fragm	307	18	1.1	3331	20	AAZ32021	Human MERT1 relate
C 235	18	1.1	420	21	AAC27182	Human secreted pro	308	18	1.1	3331	22	AAC90078	D86074 cDNA clone.
C 236	18	1.1	426	21	ABV35340	Human prostate exp	309	18	1.1	3936	23	AA582564	DNA encoding novel
C 237	18	1.1	438	23	ABV14088	Human prostate exp	310	18	1.1	4181	21	AAV21314	Human low adenosi
238	18	1.1	433	21	AAC24526	Human secreted pro	311	18	1.1	4181	21	AAV35192	Human adenostine re
C 239	18	1.1	453	23	ABV14247	Human prostate exp	312	18	1.1	4181	22	AAV86086	Human interleukin-
240	18	1.1	480	22	ABV89182	Escherichia coli p	313	18	1.1	4456	20	AAV57451	Human ALP encoding
241	18	1.1	533	24	ABL28982	Human ovarian canc	314	18	1.1	4456	20	AAV81748	Human ALP encoding
C 242	18	1.1	551	24	ABN22747	Human cancer relat	315	18	1.1	4492	19	AAV32553	Candida albicans C
C 243	18	1.1	574	24	ABV45454	Oligonucleotide fo	C 316	18	1.1	4511	23	AA581504	DNA encoding novel
244	18	1.1	574	24	ABV45455	Oligonucleotide fo	C 317	18	1.1	4979	23	AA581509	DNA encoding novel
C 245	18	1.1	583	23	ABV40937	Human prostate exp	318	18	1.1	5234	21	AAC81224	Human histidine do
C 246	18	1.1	583	23	ABV44031	Human prostate exp	C 319	18	1.1	5530	24	ABK31443	Signal transductio
C 247	18	1.1	583	23	ABV44171	Human prostate exp	C 320	18	1.1	5617	19	AAV57163	Partial human Notc
C 248	18	1.1	647	22	AA51083	cdNA encoding nove	C 321	18	1.1	6025	22	AA545338	Chemically pretrea
249	18	1.1	647	22	AA526892	Human cdna encodin	C 322	18	1.1	6980	24	ABL32452	Human immune syste
250	18	1.1	656	24	ABN96878	Gene #3376 used to	C 323	18	1.1	7016	22	AAK67154	Human immune syste
251	18	1.1	718	21	AAV15572	Human prostate can	C 324	18	1.1	7016	22	AAK70464	Human immune/haema
C 252	18	1.1	731	21	AAC77612	Human cancer assoc	C 325	18	1.1	7016	22	AAK74836	Human immune/haema
C 253	18	1.1	735	24	ABL64086	Breast cancer rela	C 326	18	1.1	8091	19	AAV57001	Human Notch3 CDNA.
254	18	1.1	759	21	AAC95474	Human secreted pro	327	18	1.1	8827	21	AAZ91916	Wild type (C57BL/6
255	18	1.1	771	20	AAZ15407	Human gene express	328	18	1.1	9309	21	AAC81225	Human tyrosine pho
256	18	1.1	847	21	AAC77942	Human cancer assoc	C 329	18	1.1	10322	21	AAZ46680	Blast disease--resi
257	18	1.1	873	16	AAV14851	Potato U14.1 DNA s	C 330	18	1.1	10401	18	AAV74460	Staphylococcus aur
C 258	18	1.1	873	16	AAV08747	Potato U14.1 DNA s	C 331	18	1.1	11520	24	ABA97202	CAPON genomic sequ
C 259	18	1.1	926	19	AAV53418	DNA encoding a rep	C 332	18	1.1	13953	24	AAD34465	Human phospholipas
260	18	1.1	958	23	ABV20544	Human prostate exp	C 333	18	1.1	14615	22	AA546705	Tumour suppressor
261	18	1.1	958	23	ABV20977	Human prostate exp	334	18	1.1	14661	22	ABA07306	Human pancreatic C
262	18	1.1	958	23	ABV21052	Human prostate exp	335	18	1.1	14661	22	AAK89227	Human digestive sy
263	18	1.1	958	23	ABV21056	Human prostate exp	336	18	1.1	14661	22	AAK90465	Human digestive sy
264	18	1.1	958	23	ABV21083	Human prostate exp	337	18	1.1	15630	21	AAV21317	Human low adenosi
265	18	1.1	958	23	ABV23216	Human prostate exp	338	18	1.1	15630	21	AAV51195	Human adenosine re
266	18	1.1	958	23	ABV26794	Human prostate exp	C 339	18	1.1	15881	24	ABL70144	Chemically treated
267	18	1.1	958	23	ABV26825	Human prostate exp	C 340	18	1.1	15881	24	ABL32261	Human immune syste
268	18	1.1	958	23	ABV26895	Human prostate exp	C 341	18	1.1	15881	24	AA561070	Human gene regulat
269	18	1.1	958	23	ABV26895	Human prostate exp	C 342	18	1.1	15881	24	ABK31183	Signal transductio
270	18	1.1	958	23	ABV26925	Human prostate exp	C 343	18	1.1	17131	24	ABLJ33053	Human immune syste
271	18	1.1	958	23	ABV28957	Human prostate exp	C 344	18	1.1	17527	24	ABLJ33433	Human immune syste
272	18	1.1	958	23	ABV29056	Human prostate exp	C 345	18	1.1	17527	24	AA563333	Chemically pretrea
273	18	1.1	1051	21	AAZ91918	Murine mahogany pr	346	18	1.1	17527	22	AAK80953	Human immune/haema
C 274	18	1.1	1113	20	AAZ25520	Rat galanin recept	C 347	18	1.1	19087	22	ABU32792	Human immune syste
C 275	18	1.1	1113	24	ABA01610	Rat galanin recept	C 348	18	1.1	21636	21	AAV55966	Human G13 3'-end
C 276	18	1.1	1280	19	AAV27892	Rat hypothalamic g	349	18	1.1	35465	22	AAV54723	Nucleotide sequenc
C 277	18	1.1	1280	24	AAV35828	Rat galanin recept	350	18	1.1	48254	22	ABA89141	Escherichia coli p
C 278	18	1.1	1315	22	AAV17482	Mouse chromogranin	351	18	1.1	48345	22	ABA89142	Escherichia coli p
C 279	18	1.1	1355	23	AA593651	DNA encoding novel	C 352	18	1.1	73334	24	ABL92319	Chemically treated
C 280	18	1.1	1375	19	AAV22716	MAGE-6 cDNA. Homo	C 353	18	1.1	73334	24	ABL24125	Human immune syste
C 281	18	1.1	1377	24	ABV30092	M. capsulatus gene	C 354	18	1.1	84539	24	ABL64158	Stomach cancer rel
282	18	1.1	1416	22	AAH28343	Nucleotide sequenc	C 355	18	1.1	20	24	ABL42954	Maturation/activat
283	18	1.1	1548	20	AAZ30523	Nucleotide sequenc	356	17	1.1	33	19	AAV13820	Primer for canine
284	18	1.1	1640	13	AAO32355	MAGE-3 cDNA. Homo	357	17	1.1	33	20	AAV35617	PCR primer for nuc
285	18	1.1	1640	15	AAO72480	Tumour rejection a	358	17	1.1	33	20	AAV35617	PCR primer for nuc
286	18	1.1	1640	20	AAV84116	MAGE-3 gene. Homo	359	17	1.1	33	20	AAV35617	PCR primer used to
287	18	1.1	1657	22	AA514051	Human FcR3a DNA s	C 360	17	1.1	35	19	AAV03359	PCR primer #1. Un
C 288	18	1.1	1657	22	AA514052	Human FcR3a DNA s	C 361	17	1.1	35	19	AAV13824	Synthetic human In
289	18	1.1	1731	21	AAV36924	Human FcR3b DNA s	362	17	1.1	39	20	AAV35621	Primer for canine
290	18	1.1	1848	18	AAV96346	Chimeric gene cont	363	17	1.1	39	20	AAV35621	PCR primer for nuc
291	18	1.1	1868	23	AA582337	DNA encoding novel	364	17	1.1	39	22	AAV64384	PCR primer #5. Un
292	18	1.1	2214	19	AAV22682	New DNA sequence 1	365	17	1.1	47	21	AAV65820	Human map-related
293	18	1.1	2415	21	AAV91917	Murine mahogany pr	C 366	17	1.1	65	24	ABN56157	Mouse spliced tran
C 294	18	1.1	2519	23	ABU05364	Drosophila melanog	C 367	17	1.1	66	14	AAV09157	Reverse 3p primer
295	18	1.1	2540	22	AAH33292	Human colon cancer	C 368	17	1.1	66	15	AAV056573	Reverse 3p primer
C 296	18	1.1	2620	22	AAH14529	Human cDNA sequenc	369	17	1.1	66	17	AAV35196	Universal 3' linker
C 297	18	1.1	2654	21	AAZ45671	Nucleotide sequenc	C 370	17	1.1	66	20	AAV08495	Universal 3p prime
C 298	18	1.1	2898	15	AAV02958	Mouse neural Menar	371	17	1.1	69	14	AAV049158	Reverse 5' primer
C 299	18	1.1	2930	18	AAV74353	Staphylococcus aur	372	17	1.1	69	15	AAV056574	Human 5' V kappa p
C 300	18	1.1	2936	24	ABA97200	CAPON-1 encoding s	373	17	1.1	69	20	AAV08496	5' V kappa primer.
C 301	18	1.1	2950	22	AA531006	Human diagnostic a	374	17	1.1	69	21	AAV74677	Human kappa light

375	17	1.1	69	21	AAA90430	Human V-kappa 5' P	448	17	1.1	600	24	AB059536	Human colon cancer
376	17	1.1	71	19	AAV37854	VL-lym with additl	449	17	1.1	610	21	AAC03820	Human secreted pro
377	17	1.1	96	17	AAV35203	(GLYSer)3 linker	450	17	1.1	612	24	AB037664	Oligonucleotide fo
378	17	1.1	200	21	AAA55341	Myrtaceae microsat	451	17	1.1	612	24	AB037665	Oligonucleotide fo
379	17	1.1	201	22	AAK46242	Human bone marrow	452	17	1.1	621	21	AAK51621	Arbidopsis thalia
380	17	1.1	201	22	AAI52143	Probe #20829 used	453	17	1.1	627	24	ABN92671	Staphylococcus epi
381	17	1.1	201	24	ABS20554	Human genome-deriv	454	17	1.1	633	21	AAZ80409	Human colon cancer
382	17	1.1	254	24	ABN27023	Human ORFX polynuc	455	17	1.1	633	24	AB058998	Human colon cancer
383	17	1.1	278	22	AAAL14168	Human breast cancer	456	17	1.1	636	24	AB060607	Human colon cancer
384	17	1.1	281	23	AAAL14400	DNA encoding novel	457	17	1.1	642	20	AAK22243	Human secreted pro
385	17	1.1	291	22	AAAS60514	Human cancer agent	458	17	1.1	643	24	AB059626	Human colon cancer
386	17	1.1	292	24	ABL84416	Human ovarian can	459	17	1.1	650	24	AB059991	Human colon cancer
387	17	1.1	293	24	ABL73337	Corn tassell-derive	460	17	1.1	651	22	AAK81464	Human colon cancer
388	17	1.1	294	24	ABL84280	Human ovarian can	461	17	1.1	672	21	AAA08848	Human DKR-4 DNA op
389	17	1.1	302	24	ABK93014	CDNA encoding huma	462	17	1.1	688	20	AAV86183	EST clone J546. H
390	17	1.1	303	21	AAK03325	Human secreted pro	463	17	1.1	696	21	AAK53763	Arbidopsis thalia
391	17	1.1	321	21	AAC02402	Human secreted pro	464	17	1.1	713	22	AAH21863	Mouse N-calcium ch
392	17	1.1	327	24	ABL79071	Human ovarian can	465	17	1.1	713	22	AAH03232	Human CDNA clone (
393	17	1.1	329	24	ABL79064	Human ovarian can	466	17	1.1	732	24	AB039656	Oligonucleotide fo
394	17	1.1	339	23	ABL21949	Drosophila melanog	467	17	1.1	732	24	AB039657	Oligonucleotide fo
395	17	1.1	342	21	AAC02344	Human secreted pro	468	17	1.1	735	24	AB043042	Oligonucleotide fo
396	17	1.1	344	24	AB058604	Human colon cancer	469	17	1.1	735	24	AB043043	Oligonucleotide fo
397	17	1.1	348	16	AAK26582	Human gene signatu	470	17	1.1	746	22	AAH05442	Human CDNA clone (
398	17	1.1	349	23	ABV61109	Human prostate exp	471	17	1.1	750	24	AB041322	Oligonucleotide fo
399	17	1.1	367	22	AAU17764	Human prostate can	472	17	1.1	750	24	AB041323	Oligonucleotide fo
400	17	1.1	367	22	AAU17782	Cervical cancer pr	473	17	1.1	751	22	AAI96187	Human neuroblastom
401	17	1.1	368	22	AAU10576	Human breast cancer	474	17	1.1	751	24	ABK74041	Bacillus licheniflo
402	17	1.1	370	22	AAK64503	Novel human polynu	475	17	1.1	755	18	AAV04904	Nucleotide sequenc
403	17	1.1	376	22	AAK64458	Human breast can	476	17	1.1	772	22	AAI23017	Human breast cancer
404	17	1.1	380	22	AAU17643	Human breast can	477	17	1.1	774	20	AAK33116	Human Fas ligand d
405	17	1.1	381	22	ABK09422	Human secreted pro	478	17	1.1	786	19	AAV42202	Exemplary nucleoti
406	17	1.1	391	22	AAU17651	Human breast can	479	17	1.1	798	19	AAV32623	DNA encoding a non
407	17	1.1	395	22	AAU10568	Human breast can	480	17	1.1	801	21	AAK46622	zee mays DNA fragm
408	17	1.1	405	22	AAU10689	Human breast can	481	17	1.1	807	19	AAV32622	DNA encoding a non
409	17	1.1	410	21	AAC07021	Human secreted pro	482	17	1.1	826	18	AAK48582	Human tub genomic
410	17	1.1	411	21	AAU10406	Fusarium venenatim	483	17	1.1	826	20	AAK16718	Human tub gene exo
411	17	1.1	454	22	ABAI3143	Human nervous syst	484	17	1.1	828	19	AAV42204	Exemplary nucleoti
412	17	1.1	454	24	ABN95963	Gene #2461 used fo	485	17	1.1	831	20	AAK33117	Human Fas ligand d
413	17	1.1	454	24	ABK64562	Human benign prost	486	17	1.1	843	20	AAZ06685	Wild type Fas lig
414	17	1.1	454	24	ABU62393	Colion adenocarcino	487	17	1.1	843	20	AAK33118	Human Fas ligand d
415	17	1.1	456	21	AAK77480	Human ORFX ORF3035	488	17	1.1	846	17	AAK09677	Human Fas ligand d
416	17	1.1	459	21	AAK38332	Zea mays DNA fragm	489	17	1.1	846	18	AAK85236	Human Fas ligand g
417	17	1.1	475	24	AB057995	Human colon cancer	490	17	1.1	846	19	AAV42201	Exemplary nucleoti
418	17	1.1	485	22	AAK33297	Human bone marrow	491	17	1.1	846	21	AAAI0474	Human Fas ligand (
419	17	1.1	485	22	AAI39086	Probe #7772 used t	492	17	1.1	860	21	AAK75704	Human Fas ligand (
420	17	1.1	485	24	ABK08130	Human genome-deriv	493	17	1.1	861	21	AAK47749	Human Fas ligand d
421	17	1.1	486	24	AB058906	Human colon cancer	494	17	1.1	864	19	AAV42203	Exemplary nucleoti
422	17	1.1	493	24	AB057676	Human breast can	495	17	1.1	868	22	AAK60792	Human cancer agent
423	17	1.1	508	22	AAU14155	Human breast can	496	17	1.1	875	21	AAK55872	Eucalyptus grandis
424	17	1.1	510	24	AB060214	Oligonucleotide fo	497	17	1.1	889	22	AAK31095	Human diagnostic a
425	17	1.1	513	24	ABQ47272	Oligonucleotide fo	498	17	1.1	894	22	AAK581442	DNA encoding novel
426	17	1.1	513	24	ABQ47273	Oligonucleotide fo	499	17	1.1	903	22	AAH99759	Human protein enco
427	17	1.1	514	22	AAH11851	Human CDNA clone (500	17	1.1	906	21	AAK42854	Arbidopsis thalia
428	17	1.1	519	16	AAK082824	GDF-7 C-terminal r	501	17	1.1	924	16	AAK03498	Human Fas ligand c
429	17	1.1	523	24	AB057737	Human colon cancer	502	17	1.1	924	21	AAK50781	Arbidopsis thalia
430	17	1.1	528	24	ABQ49916	Oligonucleotide fo	503	17	1.1	961	23	ABV30115	Human prostate exp
431	17	1.1	528	24	ABQ49917	Oligonucleotide fo	504	17	1.1	962	22	AAK02902	Human pregnane x r
432	17	1.1	532	24	AB059247	Human colon cancer	505	17	1.1	964	21	AAK50094	Arbidopsis thalia
433	17	1.1	534	23	ABV54457	Human prostate exp	506	17	1.1	967	21	AAK53290	Arbidopsis thalia
434	17	1.1	538	24	AB033778	Oligonucleotide fo	507	17	1.1	972	19	AAV42194	Nucleotide sequenc
435	17	1.1	538	24	AB033779	Oligonucleotide fo	508	17	1.1	972	20	AAK35963	Nucleotide sequenc
436	17	1.1	549	22	AAK85423	Human immune/haema	509	17	1.1	972	22	AAK08454	Human Fas ligand
437	17	1.1	559	24	AB058813	Human colon cancer	510	17	1.1	1006	24	ABQ22212	Oligonucleotide fo
438	17	1.1	562	24	AB053802	Oligonucleotide fo	511	17	1.1	1006	24	ABQ22213	Oligonucleotide fo
439	17	1.1	562	24	AB053803	Oligonucleotide fo	512	17	1.1	1006	24	ABQ22213	Oligonucleotide fo
440	17	1.1	566	24	AB057760	Human colon cancer	513	17	1.1	1014	21	AAK42729	Arbidopsis thalia
441	17	1.1	573	22	AAU23030	Human breast can	514	17	1.1	1026	21	AAK52278	Arbidopsis thalia
442	17	1.1	573	22	AAK41079	CDNA encoding nove	515	17	1.1	1051	22	AAH99359	Human protein enco
443	17	1.1	577	22	ABAI18956	Human nervous syst	516	17	1.1	1101	24	ABK31755	DNA encoding novel
444	17	1.1	577	22	ABAI18957	Human nervous syst	517	17	1.1	1143	22	AAK31118	Human diagnostic a
445	17	1.1	583	24	AB060661	Human colon cancer	518	17	1.1	1161	24	AB072605	Human MDR1 encodin
446	17	1.1	597	22	AB070788	Cervical cancer pr	519	17	1.1	1190	21	AAK50795	Arbidopsis thalia
447	17	1.1	598	24	AB059539	Human colon cancer	520	17	1.1	1192	21	AAK41980	Arbidopsis thalia

521	17	1.1	1200	23	AAS92828	DNA encoding novel	594	17	1.1	2207	23	ABLO3559	Drosophila melanog
522	17	1.1	1203	16	AAO96223	Murine mvl protein	595	17	1.1	2253	21	AAC99127	Human pancreatic c
523	17	1.1	1203	18	AAO9396	Murine BMP-12 homo	596	17	1.1	2254	20	AAK22780	Human SOCS18 CDNA
524	17	1.1	1203	22	AAD18335	Murine partial mvl	597	17	1.1	2254	20	AAK22774	Human SOCS18 CDNA
525	17	1.1	1205	24	ABN95154	Gene #1652 used to	598	17	1.1	2260	21	AAC53265	Arabidopsis thaliana
526	17	1.1	1205	24	ABL67199	Thyroid cancer rel	599	17	1.1	2261	21	AAC59294	Human secreted pro
527	17	1.1	1206	24	ABL65952	Prostate cancer re	600	17	1.1	2293	24	ABK33626	CDNA encoding huma
528	17	1.1	1214	22	AAS26402	Human cDNA encodin	601	17	1.1	2294	24	AAA37058	Human PRO1305 (UNO
529	17	1.1	1236	24	ABO29236	Oligonucleotide fo	602	17	1.1	2294	22	AAS46066	Human DNA encoding
530	17	1.1	1236	24	ABO29237	Oligonucleotide fo	603	17	1.1	2294	22	AAF54307	DNA encoding prole
531	17	1.1	1290	21	AAC46337	Arabidopsis thalia	604	17	1.1	2294	23	ABL20407	Drosophila melanog
532	17	1.1	1293	21	AAC48898	Arabidopsis thalia	605	17	1.1	2339	23	ABL21948	Drosophila melanog
533	17	1.1	1294	21	AAC42058	Arabidopsis thalia	606	17	1.1	2373	23	AAS65199	DNA encoding novel
534	17	1.1	1306	24	ABO33670	Oligonucleotide fo	607	17	1.1	2387	23	ABL23408	Drosophila melanog
535	17	1.1	1305	24	ABO33671	Oligonucleotide fo	608	17	1.1	2428	22	AAH98381	Human EST-derived
536	17	1.1	1348	22	AAS22662	Human cDNA encodin	609	17	1.1	2428	22	AAH98381	Human EST-derived
537	17	1.1	1371	21	AAS92830	DNA encoding novel	610	17	1.1	2435	16	AAO94155	Human Fas ligand g
538	17	1.1	1389	21	AAC35350	Arabidopsis thalia	611	17	1.1	2457	23	ABL26805	Drosophila melanog
539	17	1.1	1402	22	AAK52310	Human polynucleoti	612	17	1.1	2469	23	ABL11239	Drosophila melanog
540	17	1.1	1408	22	AAK53294	DNA encoding an in	613	17	1.1	2483	22	AAH15854	Human cDNA sequenc
541	17	1.1	1422	20	AAK59568	SCD4-SCRV(17b) HIV	614	17	1.1	2497	24	AAS62533	CDNA sequence #320
542	17	1.1	1440	21	AAK54045	DNA encoding novel	615	17	1.1	2595	22	AAH17091	Hexapeptide dupli
543	17	1.1	1536	23	AAS70284	DNA encoding novel	616	17	1.1	2670	22	AAH46197	Human Zntir2 CDNA
544	17	1.1	1545	22	AAS22858	Human cDNA encodin	617	17	1.1	2687	21	AAK50101	Human secreted pro
545	17	1.1	1572	22	AAS45266	Human cDNA encoding	618	17	1.1	2694	22	AAD07774	Human polynucleoti
546	17	1.1	1587	20	AAK06840	Streptococcus bran	619	17	1.1	2694	24	ABL90740	Human polynucleoti
547	17	1.1	1586	24	ABN71188	Streptococcus poly	620	17	1.1	2801	23	ABL03415	Drosophila melanog
548	17	1.1	1730	22	AAS25963	Human cDNA encodin	621	17	1.1	2802	20	AAK56243	Human vitamin D re
549	17	1.1	1757	24	ABO13658	Oligonucleotide fo	622	17	1.1	2850	20	AAK78808	Human nkr7-1 CDNA
550	17	1.1	1757	24	ABO13659	Oligonucleotide fo	623	17	1.1	2967	23	ABL04125	Drosophila melanog
551	17	1.1	1777	22	AAC85111	Maize MST-like pro	624	17	1.1	3023	24	ABA02198	Mouse C/EBP alpha-
552	17	1.1	1778	24	ABO45204	Oligonucleotide fo	625	17	1.1	3081	23	AAS90367	DNA encoding novel
553	17	1.1	1778	24	ABO45205	Oligonucleotide fo	626	17	1.1	3086	11	AAO06470	Sequence encoding
554	17	1.1	1790	15	AAV53297	Human Fas ligand c	627	17	1.1	3089	16	AAT05572	MEK3 CDNA. Mus s
555	17	1.1	1790	15	AAV53294	Fas Ligand CDNA.	628	17	1.1	3089	19	AAV22678	CDNA encoding a mi
556	17	1.1	1798	24	ABN69616	Gene #3414 used to	629	17	1.1	3089	20	AAZ31879	Mitogen ERK kinase
557	17	1.1	1804	24	ABN66757	Eukaryotic initiat	630	17	1.1	3089	20	AAV45616	MEK3 protein codi
558	17	1.1	1831	24	ABN67642	Streptococcus poly	631	17	1.1	3089	21	AAA49224	DNA encoding novel
559	17	1.1	1841	16	AAO91311	Human Fas-l gene.	632	17	1.1	3085	24	ABA041581	Sequence encoding
560	17	1.1	1841	20	AAK24879	Human Fas ligand	633	17	1.1	3108	24	ABA041581	MEK3 CDNA. Mus s
561	17	1.1	1841	20	AAK24879	Human Fas ligand	634	17	1.1	3128	24	ABL63726	Human PEl045 prote
562	17	1.1	1843	17	AAT38308	Human B-cell trans	635	17	1.1	3128	24	ABL64118	Breast cancer rela
563	17	1.1	1843	15	AAV32201	Human B-cell trans	636	17	1.1	3128	24	ABL64958	Lung cancer relate
564	17	1.1	1843	15	AAZ90056	Human B-cell trans	637	17	1.1	3128	24	ABL65643	Lung cancer relate
565	17	1.1	1843	22	AAO05296	Human B-cell trans	638	17	1.1	3128	24	ABL66296	Lung cancer relate
566	17	1.1	1883	22	AAK51739	Human polynucleoti	639	17	1.1	3128	24	ABL68072	Ovary cancer relat
567	17	1.1	1889	23	ABL06771	Drosophila melanog	640	17	1.1	3146	22	AAH23110	Osteoarthritis lis
568	17	1.1	1890	19	AAV39009	Nucleotide sequenc	641	17	1.1	3176	22	AAH18597	Human CDNA sequenc
569	17	1.1	1890	21	AAK33187	Human FAS CDNA seq	642	17	1.1	3200	22	AAK82101	Human immune/haema
570	17	1.1	1890	24	ABK63855	DNA encoding a hum	643	17	1.1	3204	24	AAD30572	Human protease, PR
571	17	1.1	1890	24	ABK63855	Human cDNA differe	644	17	1.1	3243	20	AAK59974	DNA encoding an in
572	17	1.1	1898	22	AAH13655	Human Fas locus HU	645	17	1.1	3258	22	AAE27797	Human TANGO 378 co
573	17	1.1	1905	17	AAT29986	Human cDNA sequenc	646	17	1.1	3276	23	ABL06201	Drosophila melanog
574	17	1.1	1935	17	AAZ25071	Human Fas ligand g	647	17	1.1	3294	22	AAE25735	Tobacco invertase
575	17	1.1	1945	20	AAK52723	Human MEK3 nucleot	648	17	1.1	3312	22	AAK505659	Drosophila mutant
576	17	1.1	1945	22	AAK52723	Human polynucleoti	649	17	1.1	3323	22	AAK546169	Human DNA encoding
577	17	1.1	1955	23	ABV25000	Human prostate exp	650	17	1.1	3327	24	ABK84437	Human CDNA differe
578	17	1.1	1955	23	ABV25000	Mouse ischaemic co	651	17	1.1	3327	24	ABN96935	Gene #3433 used to
579	17	1.1	1968	24	AB195429	Drosophila melanog	652	17	1.1	3332	20	AAZ25074	Colon adenocarcino
580	17	1.1	1980	23	ABV25278	Human prostate exp	653	17	1.1	3332	20	AAZ25074	Murine MEK3 nucle
581	17	1.1	1983	21	ABV77895	Human cancer assoc	654	17	1.1	3342	22	AAV55657	RAG-1 gene. Mus s
582	17	1.1	1983	24	ABO54163	Human ovarian anti	655	17	1.1	3360	24	AAZ24960	Human G-protein co
583	17	1.1	2004	24	AAD39042	Human HIF-3 DNA.	656	17	1.1	3393	22	AAE90612	Human secretin-11k
584	17	1.1	2013	23	AAS81444	DNA encoding novel	657	17	1.1	3397	22	ABA99888	Human CD24 DNA SBO
585	17	1.1	2031	23	AAS68609	DNA encoding novel	658	17	1.1	3397	24	ABA99888	Human CD24 DNA SBO
586	17	1.1	2035	21	AAC76666	Human ORFX ORF221	659	17	1.1	3416	21	AAZ52247	Maize glycine-rich
587	17	1.1	2076	22	AAD08430	Human secreted pro	660	17	1.1	3467	20	AAK12959	Enterococcus faeca
588	17	1.1	2082	22	AAH14706	Human cDNA sequenc	661	17	1.1	3600	23	ABL11429	Drosophila melanog
589	17	1.1	2087	24	AAD04056	Human carboxyleste	662	17	1.1	3684	24	ABK43938	Human cDNA encodin
590	17	1.1	2101	21	AAD00680	Human Hydrolase pr	663	17	1.1	3700	22	AAK18886	Growth hormone 1 g
591	17	1.1	2108	23	AAS87886	DNA encoding novel	664	17	1.1	3703	22	AAE87636	Human RecO5 beta D
592	17	1.1	2172	21	AAC42733	Arabidopsis thalia	665	17	1.1	3730	23	ABL13240	Drosophila melanog
593	17	1.1	2181	23	AAS52820	Enterococcus faeca	666	17	1.1	3776	22	AAD08405	Human secreted pro

C 667	17	1.1	3824	21	AAA6341	CDNA encoding a no	C 740	17	1.1	12693	22	ABA20625	Human nervous syst
C 668	17	1.1	AS21514	22	AS21514	Human CDNA sequenc	C 741	17	1.1	12693	22	AAK79994	Human immune/haema
C 669	17	1.1	3824	24	AB195693	Human angiotensin	C 742	17	1.1	13123	22	AA104954	Human reproductive
C 670	17	1.1	3824	24	AB188204	Human PRO1887 CDNA	C 743	17	1.1	13123	23	AB197848	Human testicular a
C 671	17	1.1	3824	24	ABK3640	CDNA encoding huma	C 744	17	1.1	13407	22	AAK89955	Human digestive sy
C 672	17	1.1	4110	22	AAK70425	Human immune/haema	C 745	17	1.1	13857	22	AA158199	Human polynucleoti
C 673	17	1.1	4135	22	AAE25742	Tobacco promoter/1	C 746	17	1.1	13865	20	AA113137	Human polynucleoti
C 674	17	1.1	4219	23	AB120404	Drosophila melanog	C 747	17	1.1	14156	20	AA559589	Enterococcus faeca
C 675	17	1.1	4312	22	AAE25736	Tobacco invertase	C 748	17	1.1	14255	14	AAO43526	Propionibacterium
C 676	17	1.1	4319	22	AA136846	Human musculoskele	C 749	17	1.1	14255	16	AAO75181	ALT-1 gene cDNA.
C 677	17	1.1	4328	23	AB111238	Drosophila melanog	C 750	17	1.1	14255	19	AAV20477	Human ALL-1/AF-4 o
C 678	17	1.1	4570	23	AB103558	Drosophila melanog	C 751	17	1.1	14255	24	AB167248	Thyroid cancer rel
C 679	17	1.1	4651	24	ABK93534	Human breast speci	C 752	17	1.1	14926	19	AAV62156	HSV-2 strain SB5 C
C 680	17	1.1	4719	22	AAAD18822	Human kinase (PKIN	C 753	17	1.1	15951	24	AB170373	Chemically treated
C 681	17	1.1	4740	10	AAAN91159	DNA sequence downs	C 754	17	1.1	15951	24	AB133680	Human immune syste
C 682	17	1.1	4755	23	AB101896	Drosophila melanog	C 755	17	1.1	15951	24	AB134580	Human metastasis a
C 683	17	1.1	4857	23	AB103544	Drosophila melanog	C 756	17	1.1	17156	23	AB107408	Drosophila melanog
C 684	17	1.1	4996	23	AB126804	Drosophila melanog	C 757	17	1.1	17293	24	AB170126	Chemically treated
C 685	17	1.1	5044	23	AB106612	Drosophila melanog	C 758	17	1.1	17293	24	AA561058	Human gene regulat
C 686	17	1.1	5066	23	AB103414	Drosophila melanog	C 759	17	1.1	17293	24	ABK31171	Signal transductio
C 687	17	1.1	5093	16	AAO99876	KIP1 coding sequen	C 760	17	1.1	17687	22	AA542069	Genomic sequence #
C 688	17	1.1	5093	20	AAV71909	S. cerevisiae KIP1	C 761	17	1.1	19815	22	AA542064	Genomic sequence #
C 689	17	1.1	5163	22	AAE44658	Novel protein kin	C 762	17	1.1	19942	22	AAK87416	Human immune/haema
C 690	17	1.1	5191	21	AAE20989	Human low adenosin	C 763	17	1.1	21252	20	AA113031	Enterococcus faeca
C 691	17	1.1	5191	21	AAK34867	Human adenosine re	C 764	17	1.1	23210	22	AAE28530	Genomic fragment #
C 692	17	1.1	5191	24	ABK83976	Human CDNA differe	C 765	17	1.1	23914	23	AB120258	Drosophila melanog
C 693	17	1.1	5191	24	AB167673	Oesophagus cancer	C 766	17	1.1	24757	22	AA527687	DNA encoding novel
C 694	17	1.1	5264	23	AB106770	Drosophila melanog	C 767	17	1.1	24757	22	AA533481	DNA encoding human
C 695	17	1.1	5283	24	AB133892	Human immune syste	C 768	17	1.1	25975	22	AA104955	Human reproductive
C 696	17	1.1	5394	23	AB104124	Drosophila melanog	C 769	17	1.1	25975	23	AB197849	Human testicular a
C 697	17	1.1	5461	24	AB06978	Human angiotensin	C 770	17	1.1	32132	22	AA135843	Human musculoskele
C 698	17	1.1	5461	24	AB132999	Human immune syste	C 771	17	1.1	32132	22	AA107060	Human reproductive
C 699	17	1.1	5845	22	AAK75705	Human immune/haema	C 772	17	1.1	32169	22	ABA14358	Human nervous syst
C 700	17	1.1	5987	24	AB067101	Human angiotensin	C 773	17	1.1	33769	22	ABK82622	Human HBV gene reg
C 701	17	1.1	5987	24	AB133562	Human immune syste	C 774	17	1.1	33769	24	ABK22781	Human hbv gene ma
C 702	17	1.1	6051	22	AA546604	Tumour suppressor	C 775	17	1.1	36159	24	ABN85329	Human kinase gene.
C 703	17	1.1	6051	24	AB133851	Human immune syste	C 776	17	1.1	42573	23	AB128622	Drosophila melanog
C 704	17	1.1	6079	23	AB111428	Drosophila melanog	C 777	17	1.1	44456	23	AAK70336	AB109962
C 705	17	1.1	6195	24	AB132591	Human immune syste	C 778	17	1.1	50885	22	AAK70336	Human immune/haema
C 706	17	1.1	6418	24	AB132322	Human immune syste	C 779	17	1.1	73334	24	AB192318	Chemically treated
C 707	17	1.1	6418	24	AA561073	Human gene regulat	C 780	17	1.1	73334	24	AB134124	Human immune syste
C 708	17	1.1	6607	24	AB134110	Human immune syste	C 781	17	1.1	109201	24	AB088125	Human osteoblast d
C 709	17	1.1	6666	12	AAO10416	Mutant protease ge	C 782	17	1.1	110096	24	ABN95044	Gene #1542 used to
C 710	17	1.1	6675	12	AAO10414	Mutant protease ge	C 783	17	1.1	113515	24	AB134174	Human immune syste
C 711	17	1.1	6675	12	AAO10415	Mutant protease ge	C 784	17	1.1	117213	19	AAV62176	HSV-2 strain SB5 C
C 712	17	1.1	6675	12	AAO10411	Mutant protease ge	C 785	17	1.1	139389	24	ABK84795	Human CDNA differe
C 713	17	1.1	6675	12	AAO10412	Mutant protease ge	C 786	17	1.1	159400	24	AB088126	Human osteoblast d
C 714	17	1.1	6675	12	AAO10413	Mutant protease ge	C 787	17	1.1	183999	22	AAE92831	Human ABC1 genomic
C 715	17	1.1	6675	12	AAO10417	Mutant protease ge	C 788	17	1.1	236303	22	AA511614	Human genomic DNA
C 716	17	1.1	6693	12	AAO10871	Mutant protease ge	C 789	17	1.1	349960	18	AAE86431	Pyrococcus abyssi
C 717	17	1.1	6711	12	AAO10870	Mutant protease ge	C 790	17	1.1	580073	22	AAE58840	Mycoplasma genital
C 718	17	1.1	6907	24	AB132566	Human immune syste	C 791	17	1.1	1230025	20	AAK91990	Nucleotide sequenc
C 719	17	1.1	6907	24	ABK71094	Human immune/haema	C 792	17	1.1	1503900	22	AAK95240	Human neureregulin-1
C 720	17	1.1	7185	22	AAH21860	Mouse N-calcium ch	C 793	17	1.1	1664976	19	AAV21209	Methanococcus jann
C 721	17	1.1	7215	23	AB106200	Drosophila melanog	C 794	17	1.1	4403765	22	AA199683	Myobacterium tube
C 722	17	1.1	7332	23	AB107409	Drosophila melanog	C 795	17	1.1	4403765	22	AA199683	Myobacterium tube
C 723	17	1.1	7920	22	ABK16924	Human nervous syst	C 796	17	1.1	4411529	22	AA199682	Myobacterium tube
C 724	17	1.1	8116	22	AAE88026	Human immune/haema	C 797	17	1.1	4411529	22	AA199682	Myobacterium tube
C 725	17	1.1	8144	22	AA546633	Chemically treated	C 798	17	1.1	4411529	22	AA199682	Myobacterium tube
C 726	17	1.1	8196	24	AB170261	Human immune syste	C 799	17	1.1	4411529	22	AA199682	Myobacterium tube
C 727	17	1.1	8196	24	AB133092	Human immune syste	C 800	17	1.1	4411529	22	AA199682	Myobacterium tube
C 728	17	1.1	8196	24	AB133092	Human immune syste	C 801	17	1.1	4411529	22	AA199682	Myobacterium tube
C 729	17	1.1	8389	22	AAK69590	Human immune/haema	C 802	17	1.1	4411529	22	AA199682	Myobacterium tube
C 730	17	1.1	8927	23	ABV25552	Human prostate exp	C 803	17	1.1	4411529	22	AA199682	Myobacterium tube
C 731	17	1.1	9539	23	AB115474	Drosophila melanog	C 804	17	1.1	4411529	22	AA199682	Myobacterium tube
C 732	17	1.1	9703	22	AA533480	DNA encoding human	C 805	17	1.1	4411529	22	AA199682	Myobacterium tube
C 733	17	1.1	9813	20	AAK13059	Enterococcus faeca	C 806	17	1.1	4411529	22	AA199682	Myobacterium tube
C 734	17	1.1	10254	24	AB067045	Human angiotensin	C 807	17	1.1	4411529	22	AA199682	Myobacterium tube
C 735	17	1.1	10838	22	AA136333	Human musculoskele	C 808	17	1.1	4411529	22	AA199682	Myobacterium tube
C 736	17	1.1	11052	24	ABK39985	Human chemically p	C 809	17	1.1	4411529	22	AA199682	Myobacterium tube
C 737	17	1.1	11133	23	AB120406	Drosophila melanog	C 810	17	1.1	4411529	22	AA199682	Myobacterium tube
C 738	17	1.1	11907	15	AAO45339	CDNA encoding htlx	C 811	17	1.1	4411529	22	AA199682	Myobacterium tube
C 739	17	1.1	12042	23	AA576999	DNA encoding novel	C 812	17	1.1	4411529	22	AA199682	Myobacterium tube

c 813	15	55	21	AAA90429	Human JH region/1	886	15	1.0	286	22	AAI19454	Human breast cance
814	15	65	24	ABN29377	Rat spliced transc	c 887	15	1.0	289	24	ABL76563	Coron tassel-deriv
815	15	1.0	66	ABT35195	(Gli4Ser)3 linker	c 888	16	1.0	292	21	AAAC6225	Nucleotide sequenc
816	15	1.0	75	AAA05659	Oligonucleotide SE	c 889	16	1.0	292	21	AAAC63995	Human TNFR homolo
817	15	1.0	78	AAAT35202	(Gli4Ser)3 linker	c 890	16	1.0	292	22	AAAC65995	Human TNFR homolo
818	15	1.0	81	AAA05700	Oligonucleotide SE	c 891	16	1.0	294	22	AAI04343	Human reproductive
819	15	1.0	87	AAA05701	Oligonucleotide SE	c 892	16	1.0	297	23	ABV00556	Human prostate exp
820	15	1.0	87	AAAS09505	Human anti-p18	c 893	16	1.0	300	21	AAA01285	Human colon cancer
c 821	15	1.0	88	ABA76590	Human foetal liver	894	15	1.0	300	24	ABL38477	Human colon tumour
c 822	15	1.0	88	AAI57389	Probe #26075 used	895	16	1.0	303	22	AAI15621	Human breast cance
823	15	1.0	96	AAAF6821	Codon-optimised HP	896	16	1.0	303	22	AAI24465	Human breast cance
824	15	1.0	112	AAAT2617	Human foetal liver	897	16	1.0	304	24	ABL62978	Breast cancer rela
825	15	1.0	112	ABA38327	Probe #16793 for g	898	16	1.0	305	22	AAI09067	Human breast cance
826	15	1.0	112	AAK21046	Human brain expres	899	16	1.0	310	19	AAV19194	Human XAG growth f
827	15	1.0	112	AAK47198	Human bone marrow	900	16	1.0	310	22	AAAF63353	Gene #3146 used to
828	15	1.0	112	AAI25875	Probe #15808 for g	901	16	1.0	315	24	ABV66273	Prostate cancer re
829	15	1.0	112	AAI53034	Probe #21720 used	c 902	16	1.0	317	22	AAK53730	Murine transcripti
830	15	1.0	112	AAAT35034	Human genome-deriv	903	16	1.0	318	22	ABA47986	Human breast cell
831	15	1.0	117	AAAT17686	Functional biotin	904	16	1.0	318	22	ABA55873	Human foetal liver
832	15	1.0	117	AAAT17685	Functional biotin	905	16	1.0	318	22	ARA32959	Probe #11425 for g
833	15	1.0	135	ABT79893	Human ovarian canc	906	16	1.0	318	22	AAK14284	Human brain expres
834	15	1.0	143	AAAS0858	Human breast cell	907	16	1.0	318	22	AAK40016	Human bone marrow
835	15	1.0	143	AAAF6831	Human foetal liver	908	16	1.0	318	22	AAI20805	Probe #10738 for g
836	15	1.0	143	ABA35782	Probe #14248 for g	909	16	1.0	318	22	AAI46035	Human lung tumour
837	15	1.0	143	AAK17167	Human brain expres	910	16	1.0	318	22	AAI06513	cDNA encoding clon
838	15	1.0	143	AAAT17013	Human genome-deriv	911	16	1.0	318	24	ABSI4102	AA233726
c 839	15	1.0	148	AAAT74562	Human foetal liver	912	16	1.0	326	24	ABL78975	AA233726
c 840	15	1.0	148	AAK23031	Human brain expres	913	16	1.0	327	21	AAAC46352	Human genome-deriv
c 841	15	1.0	148	AAK49206	Human bone marrow	914	16	1.0	327	21	AAAC46352	Human genome-deriv
c 842	15	1.0	148	AAI55042	Probe #23728 used	c 915	16	1.0	328	22	AAI00540	Arabidopsis thalia
843	15	1.0	155	AAAT70556	Human foetal liver	c 916	16	1.0	328	22	AAAF68313	Human reproductive
844	15	1.0	155	AAK18802	Human brain expres	c 917	16	1.0	328	24	ABK38224	Human lung tumour
845	15	1.0	155	AAK44740	Human bone marrow	918	16	1.0	329	20	AA233726	cDNA encoding clon
846	15	1.0	155	AAI50718	Probe #19404 used	919	16	1.0	330	21	AAAO9013	AA233726
847	15	1.0	155	AAAT18978	Human genome-deriv	c 920	16	1.0	339	22	AAAS37909	AA233726
c 848	15	1.0	165	AAAT6564	Human breast cell	c 921	16	1.0	340	24	ABN25815	Novel human diago
c 849	15	1.0	165	AAAT35641	Probe #12107 for g	c 922	16	1.0	341	21	AAAF11099	Human ORF1976 cDNA
c 850	15	1.0	165	AAK15001	Human brain expres	c 923	16	1.0	341	21	AAZ42802	Fusarium venenatum
c 851	15	1.0	165	AAK40733	Human bone marrow	c 924	16	1.0	343	24	ABL83220	Human 5' EST isola
c 852	15	1.0	165	AAI46787	Probe #15473 used	c 925	16	1.0	344	22	AAAF65755	Human HCRFR2 exon
c 853	15	1.0	165	AAI07193	Probe #7184 used t	c 926	16	1.0	347	24	ABO85877	Arabidopsis thalia
c 854	15	1.0	167	AAO61010	Human brain expres	c 927	16	1.0	347	23	ABV58778	Human prostate exp
855	15	1.0	167	AAAT76232	Human foetal liver	c 928	16	1.0	351	24	ABN77029	Human ORF1976 cDNA
856	15	1.0	167	ABA40775	Probe #19241 for g	c 929	16	1.0	359	22	AAK58271	Human immune/haema
857	15	1.0	167	AAI27916	Probe #17849 for g	c 930	16	1.0	363	24	ABN24829	Human ORF1976 cDNA
858	15	1.0	167	AAI56901	Probe #25587 used	c 931	16	1.0	370	20	AAV87315	EST clone Bp780.
c 859	15	1.0	201	AAK91035	Human digestive sy	c 932	16	1.0	372	21	AAH30739	Human colon cancer
c 860	15	1.0	201	AAAT32070	Human liver associ	c 933	16	1.0	373	22	ABA44420	Human breast cell
c 861	15	1.0	201	AAAT32070	Human liver associ	c 934	16	1.0	373	22	ABA54671	Human foetal liver
862	15	1.0	221	AAI20456	Human breast cance	c 935	16	1.0	373	22	ABA24453	Probe #2919 for ge
c 863	15	1.0	222	AAI17035	Human breast cance	c 936	16	1.0	373	22	AAK02958	Human brain expres
864	15	1.0	222	AAI18287	Human breast cance	c 937	16	1.0	373	22	AAK28403	Human bone marrow
865	15	1.0	222	AAI18287	Human breast cance	c 938	16	1.0	373	22	AAI12958	Probe #2801 for ge
866	15	1.0	223	AAI11558	Human breast cance	c 939	16	1.0	373	22	AAI34328	Probe #3014 used t
c 867	15	1.0	240	AAAT3454	Human breast cance	c 940	16	1.0	373	22	AAI02888	Probe #2879 used t
868	15	1.0	247	AAAT3454	Cat flea hindgut a	c 941	16	1.0	374	21	AAAS02912	Human genome-deriv
c 869	15	1.0	247	AAAT3454	Cat flea hindgut a	c 942	16	1.0	374	24	AAAS05960	Human genome-deriv
c 870	15	1.0	249	AAAT3454	Cat flea hindgut a	c 943	16	1.0	376	22	AAH12330	Human CDNA clone (
c 871	15	1.0	251	AAAT3454	Human breast cance	c 944	16	1.0	378	23	AAAS58105	Human CDNA clone (
872	15	1.0	257	AAAT3454	Human secreted pro	c 945	16	1.0	387	22	AAAT70991	Human foetal liver
873	15	1.0	258	AAAT3454	Ovary cancer relat	c 946	16	1.0	387	22	AAAT3454	Probe #15875 for g
874	15	1.0	259	AAAT3454	Human colon tumour	c 947	16	1.0	387	22	AAAT3454	Human brain expres
c 875	15	1.0	259	AAAT3454	Polynucleotide sequenc	c 948	16	1.0	387	22	AAAT3454	Human prostate exp
c 876	15	1.0	261	AAAT3454	Nucleotide sequenc	c 949	16	1.0	387	22	AAAT3454	Human colon cancer
c 877	15	1.0	264	AAAT3454	CDNA #1488 encodin	c 950	16	1.0	387	22	AAAT3454	Human breast cance
878	15	1.0	264	AAAT3454	Human foetal liver	c 951	16	1.0	387	22	AAAT3454	Human breast cance
879	15	1.0	264	AAAT3454	Probe #15949 for g	c 952	16	1.0	388	21	AAAT3454	Human breast cance
880	15	1.0	264	AAAT3454	Human brain expres	c 953	16	1.0	390	20	AAAT3454	Human breast cance
881	15	1.0	264	AAAT3454	Human bone marrow	c 954	16	1.0	390	20	AAAT3454	Human breast cance
882	15	1.0	264	AAAT3454	Probe #20035 used	c 955	16	1.0	390	20	AAAT3454	Human breast cance
883	15	1.0	267	AAAT3454	Human genome-deriv	c 956	16	1.0	391	15	AAAT3454	Human genome-deriv
884	15	1.0	278	AAAT3454	Human breast cance	c 957	16	1.0	392	24	AAAT3454	5' region of porc
885	15	1.0	282	AAAT3454	Human secreted pro	c 958	16	1.0	400	22	AAAT3454	Human ORF2788 cDNA
				AAI19842	Human breast cance						ABA45302	Human breast cell

PR	23-MAY-1996:	96JP-012B104.
PR	08-NOV-1995:	95JP-026B729.
XX		
PA	(TORA) TORAY IND INC.	
XX		
DR	WPI: 1998-174914/16.	
DR	P-PSDB: AAW41791.	
XX		
PT	Canine interleukin 12 - comprises p40 and p35 subunits; useful in	
PT	veterinary medicine, e.g. antitumour, antiviral and vaccine adjuvant	
PT	activities are expected	
XX		
PS	Claim 10; Pages 10-11; 12pp; Japanese.	
XX		
CC	The present sequence encodes a canine interleukin-12 (IL-12) p40	
CC	subunit. A canine IL-12 comprising a p40 and p35 subunit is capable	
CC	of inducing an antiviral activating factor and the expression of	
CC	Class II MHC molecules in canine tumour cells, stimulating	
CC	proliferation of canine blastogenic lymphocytes and activating	
CC	canine leukocytes to inhibit canine tumour cells. The canine IL-12	
CC	can be used in veterinary medicines, e.g. antitumour, antiviral and	
CC	vaccine adjuvant activities are expected.	
XX		
SO	Sequence 990 BP; 279 A; 244 C; 249 G; 218 T; 0 other:	
	Query Match	60.9%; Score 974; DB 19; Length 990;
	Best local Similarity 100.0%; Pred. No. 0;	
	Matches 974; Conservative 100; Mismatches 0; Indels 0; Gaps 0;	
OY	7 CCTAGCGATTGTCATCTCCGTTTCCGTCGTTTCTGCTGCGCTCCCTCATGGCC	66
DB	7 CCTAGCGATTGTCATCTCCGTTTCCGTCGTTTCTGCTGCGCTCCCTCATGGCC	66
QY	67 ATATGGGAAGTGGAGAAAGATGTTATGCTGTAGAGTTGGACTGGCACCCGATGCCCC	126
DB	67 ATATGGGAAGTGGAGAAAGATGTTATGCTGTAGAGTTGGACTGGCACCCGATGCCCC	126
OY	127 GGAGAAATGCTGTCCTTCTACCTGCATACCCCTGGAAGAAGATGACATCATCTTGACCTCA	186
DB	127 GGAGAAATGCTGTCCTTCTACCTGCATACCCCTGGAAGAAGATGACATCATCTTGACCTCA	186
OY	187 GCGGAGACACTGTAAGTCTCTAGTTCCTGGTAAACATCTGACCATCCAAAGTCAATTT	246

307 TTGATTTCACAAAAGAAGATGGAATTTGGTCCAC

Db	307	TTGATTTCACAAAAAAGAAAGATGGAAATTTGGTCCACGTGATATCTTAAAGGACACGAAAAA	366
QY	367	TCCAAAAATAAAGATCTTTCCTGAATGTGAGGCCAAGAATTAATTCGAGCGTTTCACATGC	422
Db	367	TCCAAAAATAAAGATCTTTCCTGAATGTGAGGCCAAGAATTAATTCGAGCGTTTCACATGC	422
QY	427	TGCTGGCTGACGGCGCATCAGTACTGATTTGAAAAATTCAGTGTCAAAAGTAGCAGAGCGTTTC	486
Db	427	TGCTGGCTGACGGCGCATCAGTACTGATTTGAAAAATTCAGTGTCAAAAGTAGCAGAGCGTTTC	486
QY	487	TCGAGACCCCAAGGGGTGACACTGTGGAGACAGTACACCTTTCAGCAGAGAGGTCAGAGTGG	544
Db	487	TCGAGACCCCAAGGGGTGACACTGTGGAGACAGTACACCTTTCAGCAGAGAGGTCAGAGTGG	544
Db	487	TCGAGACCCCAAGGGGTGACACTGTGGAGACAGTACACCTTTCAGCAGAGAGGTCAGAGTGG	548
QY	547	GACACACAGGAGTTTAAGAACTATACACGTGAGTGTGCAGAGGGCAGTGGCCGGCCGCT	606
Db	547	GACACACAGGAGTTTAAGAACTATACACGTGAGTGTGCAGAGGGCAGTGGCCGGCCGCT	606
QY	607	GCCGAGGAGAGCCTTAACCATGAGCTGTGGTGTGATGCTATTTCACAAAGCTCAAGTATGAA	666
Db	607	GCCGAGGAGAGCCTTAACCATGAGCTGTGGTGTGATGCTATTTCACAAAGCTCAAGTATGAA	666

QY 667 AACTGACACGAGCATTCTTCATCAGAGACATCATCAACGACGACCCGACAAACCTG 726
|||||
Db 667 AACTGACACGAGCATTCTTCATCAGAGACATCATCAACGACGACCCGACAAACCTG 726
QY 727 CAGCTGAAGCCATTGAAAAATTCGCGACGCTGGAGGTCAGTGGGAATACCCGACAC 786
|||||
Db 727 CAGCTGAAGCCATTGAAAAATTCGCGACGCTGGAGGTCAGTGGGAATACCCGACAC 786
QY 787 TGGACACACCCGACATTCCTACTTCCTGACATTTTGCAATACAGCCGACGGGCAAGAC 846
|||||
Db 787 TGGACACACCCGACATTCCTACTTCCTGACATTTTGCAATACAGCCGACGGGCAAGAC 846
QY 847 AATAGAGAAAGAAAGATAGACTCTGCGTGACAGACCTGACCCAGGTCGTGGCCAC 906
|||||
Db 847 AATAGAGAAAGAAAGATAGACTCTGCGTGACAGACCTGACCCAGGTCGTGGCCAC 906
QY 907 AAGATGCGCAAGATCCGCGTGCAGACCCGACAGCCGCTACTATAGTTCTCGACAGCAG 966
|||||
Db 907 AAGATGCGCAAGATCCGCGTGCAGACCCGACAGCCGCTACTATAGTTCTCGACAGCAG 966
/ 967 TGGCATCTCTGTGTC 980
|||||
Db 967 TGGCATCTCTGTGTC 980
RESULT 2
AA35625
ID AA35625 standard; cDNA to mRNA; 960 bp.
XX
AC AA35625:
XX
DT 09-JUL-1999 (first entry)
XX
DE Nucleic acid encoding canine Interleukin-12 (IL-12).
XX
KW Interleukin-12; IL-12; dog; cat; immune disease; CatIL12; heterodimer;
XX
KW Tumour; skin disease; infectious disease; allergic disease; ds.
XX
OS Canis sp.
XX
FI Key Location/Qualifiers
FT 1..960
FT CDS /*Lag= a
XX
PN JP11106350-A.
XX
PD 20-APR-1999.
XX
XX 15-MAY-1998; 98JP-0133345.
XX
PR 07-AUG-1997; 97JP-0213755.
XX
PR 16-MAY-1997; 97JP-0127650.
XX
PA (TOKA) TOKAY IND INC.
XX
XX WPI: 1999-308068/26.
XX
DR P-PSDB: AAY02342.
XX
PT A prevention and treating agent containing interleukin 12 (CatIL12) -
XX
XX for prevention and treatment of dog and cat immune diseases
XX
XX Claim 1: Page 14-15; 16pp; Japanese.
XX
XX The present sequence encodes canine interleukin-12 (IL-12). The
XX
XX specification describes a method for the prevention and treatment
XX
XX of dog and cat immune diseases. The treatment used an agent comprising
XX
XX dog IL-12 (CatIL12) proteins to form a heterodimer. The agent is
XX
XX useful for preventing and treating dog and cat immune diseases,
XX
XX including tumours, skin diseases, infectious diseases and allergic
XX
XX diseases.
XX
XX Sequence 960 bp; 279 A; 244 C; 249 G; 218 T; 0 other;

Query Match 60.9%; Score 974; DB 20; Length 990;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 974; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 CCTAGCAGTTGGTCATCTCCTGATTTTCCCTGTTTTCGCGTCCTCCCTCATGGCC 66
|||||
Db 7 CCTAGCAGTTGGTCATCTCCTGATTTTCCCTGTTTTCGCGTCCTCCCTCATGGCC 66
QY 67 ATATGGGAACGTGGAGAAGATGTTTATGTTAGAGTTGGACATGGCACCCTGATGCCCC 126
|||||
Db 67 ATATGGGAACGTGGAGAAGATGTTTATGTTAGAGTTGGACATGGCACCCTGATGCCCC 126
QY 67 ATATGGGAACGTGGAGAAGATGTTTATGTTAGAGTTGGACATGGCACCCTGATGCCCC 126
|||||
Db 67 ATATGGGAACGTGGAGAAGATGTTTATGTTAGAGTTGGACATGGCACCCTGATGCCCC 126
QY 127 GGAGAAATGGTGGTCCCTGACCTGACCATGACCCCTGAAGAAGATGACATGACTTGGACCTCA 186
|||||
Db 127 GGAGAAATGGTGGTCCCTGACCTGACCATGACCCCTGAAGAAGATGACATGACTTGGACCTCA 186
QY 187 GCGCAGACCACTGAAGTCTTAGTTCTGGTAAACTGTGACCATGCAAGTCAAAAGATTTT 246
|||||
Db 187 GCGCAGACCACTGAAGTCTTAGTTCTGGTAAACTGTGACCATGCAAGTCAAAAGATTTT 246
QY 247 CGAGATGCTGGCCAGTATACCTGCCATTAAGAGAGGCAAGGTTCTGAGCCCTCATCTCTG 306
|||||
Db 247 CGAGATGCTGGCCAGTATACCTGCCATTAAGAGAGGCAAGGTTCTGAGCCCTCATCTCTG 306
QY 307 TTGATTCACAAAAAAGAGATGGAATTTGTCACCTGATATCTTAAAGCAAGACAGAAAGAA 366
|||||
Db 307 TTGATTCACAAAAAAGAGATGGAATTTGTCACCTGATATCTTAAAGCAAGACAGAAAGAA 366
QY 367 TCCAAAAATTAAGATCTTTCTGAATGTGAGGCAAAAGAAATTTATCTGACGTTTCACATGC 426
|||||
Db 367 TCCAAAAATTAAGATCTTTCTGAATGTGAGGCAAAAGAAATTTATCTGACGTTTCACATGC 426
QY 427 TGGTGGCTGACGGGCAATGACATGATGATTTGAAATTCAGTGTCAAAAGTAGAGAGGCTTC 486
|||||
Db 427 TGGTGGCTGACGGGCAATGACATGATGATTTGAAATTCAGTGTCAAAAGTAGAGAGGCTTC 486
QY 487 TCTGACCCCGCAAGGGGTACATGTGAGACAGTGAACACTTTCAGCAGAGAGGTCAGAGTG 546
|||||
Db 487 TCTGACCCCGCAAGGGGTACATGTGAGACAGTGAACACTTTCAGCAGAGAGGTCAGAGTG 546
QY 547 GACAAACAGGATTTATAGACTACACAGTGAAGTGTGAGAGGGCAGTGCCTGCCCTCT 606
|||||
Db 547 GACAAACAGGATTTATAGAGTACACAGTGAAGTGTGAGAGGGCAGTGCCTGCCCTCT 606
QY 607 GCGCAGAGAGCCCTACCCATGAGGTCGTGGTGGATGCTATTTCACAACTCAAGTATGAA 666
|||||
Db 607 GCGCAGAGAGCCCTACCCATGAGGTCGTGGTGGATGCTATTTCACAACTCAAGTATGAA 666
QY 667 AACTGACACGAGCATTCTTCATCAGAGACATCATCAACGACGACCCGACAAACCTG 726
|||||
Db 667 AACTGACACGAGCATTCTTCATCAGAGACATCATCAACGACGACCCGACAAACCTG 726
QY 727 CAGCTGAAGCCATTGAAAAATTCGCGACGCTGGAGGTCAGTGGGAATACCCGACAC 786
|||||
Db 727 CAGCTGAAGCCATTGAAAAATTCGCGACGCTGGAGGTCAGTGGGAATACCCGACAC 786
QY 787 TGGAGACACCCGACATTCCTACTTCCTGACATTTTGCAATACAGGCCGACGGGCAAGAC 846
|||||
Db 787 TGGAGACACCCGACATTCCTACTTCCTGACATTTTGCAATACAGGCCGACGGGCAAGAC 846
QY 847 AATAGAGAAAGAAAGATAGACTCTGCGTGACAGACCTGACCCAGGTCGTGGCCAC 906
|||||
Db 847 AATAGAGAAAGAAAGATAGACTCTGCGTGACAGACCTGACCCAGGTCGTGGCCAC 906
QY 907 AAGATGCGCAAGATCCGCGTGCAGACCCGACAGCCGCTACTATAGTTCTCGACAGCAG 966
|||||
Db 907 AAGATGCGCAAGATCCGCGTGCAGACCCGACAGCCGCTACTATAGTTCTCGACAGCAG 966
QY 967 TGGCATCTCTGTGTC 980
|||||
Db 967 TGGCATCTCTGTGTC 980

```
RESULT 3
AA03162
ID AAX03162 standard: cDNA to mRNA: 990 BP.
XX
XX AAX03162:
AC
XX
XX 30-MAR-1999 (first entry)
DT
XX
DE Nucleic acid encoding canine Interleukin 12.
XX
XX Canine: Interleukin 12; IL-12; feline; immunological disease; tumour;
KM skin disease; viral infection; allergic disease; breast tumour;
KM eosinophilic granuloma; epidermoid tumour; skin tumour; lipoma;
KM ochematoma; pneumoedema; skin soft pedicled soft tumour; anal tumour;
KM oclitis externa; dermatitis; eczema; fungal skin disease; pyoderma;
KM allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
KM dog parvovirus infection; distemper virus; cat plaque virus infection;
KM feline leukaemia; allergy; pollinosis; ds.
XX
XX Canis sp.
XX
XX Key Location/Qualifiers
FT CDS 1:990
FT /tag= a
FT /product= Interleukin_12
XX
XX MO9851327-A1.
XX
XX 19-NOV-1998.
XX
XX 07-MAY-1998: 98WO-JP02031.
XX
XX 16-MAY-1997: 97JP-0127690.
XX
XX (TORA ) TORAY IND INC.
XX
XX Okano F, Satoh M, Yamada K:
XX
XX WPI: 1999-070100/06.
XX
XX P-PSDB: AAW84373.
XX
XX New therapeutic and prophylactic agents - comprise
PT genetically engineered canine interleukin 12, used to treat, e.g.
PT canine and feline immunological diseases
XX
XX
XX Claim 1: Page 30-32: 45pp: Japanese.
XX
XX The present sequence encodes a canine interleukin 12 (IL-12) protein.
XX The IL-12 protein can be used in therapeutic or prophylactic agents.
XX The agents can be used to prevent and treat canine and feline
XX immunological diseases including dog and cat tumours, skin diseases,
XX viral infections and allergic diseases, especially tumours, breast
XX tumour, eosinophilic granuloma, epidermoid tumour, skin tumour, lipoma,
XX ochematoma, pneumoedema, skin soft pedicled soft tumour and anal
XX tumour; skin diseases, oclitis externa, dermatitis, eczema, fungal
XX diseases of the skin, pyoderma, allergic dermatitis, nettle rash,
XX traumatic dermatitis and hair loss; infections: dog parvovirus infection
XX and distemper virus, cat plaque virus infection and feline leukaemia, and
XX allergic diseases, e.g. pollinosis.
XX
XX
XX Sequence 990 BP: 279 A; 244 C; 249 G; 218 T; 0 other:
SQ
Query Match 60.9%; Score 974; DB 20; Length 990;
Best local Similarity 100.0%; Pred. No. 0;
Matches 974; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 127 GGAGAAATGGTGGTCTACCTGGCCATACCCCTGAGAAGATGACATCTTGGACCTCA 186
DB 127 GGAGAAATGGTGGTCTACCTGGCCATACCCCTGAGAAGATGACATCTTGGACCTCA 186
QY 187 GCGGAGAGCAGTGAAGTCTGATGTTCTGTAAACTCTGACCATTCAGTCAAGTAAAGATT 246
DB 187 GCGGAGAGCAGTGAAGTCTGATGTTCTGTAAACTCTGACCATTCAGTCAAGTAAAGATT 246
QY 247 GGAGATGCTGGCCAGTATACCTGGCATTAAGAGAGCAAGTTCGACCCGCTCAGCTCTG 306
DB 247 GGAGATGCTGGCCAGTATACCTGGCATTAAGAGAGCAAGTTCGACCCGCTCAGCTCTG 306
QY 307 TTGATTTACAAAAGAAAGATGATGATTTGGTCACCTATATCTTAAAGAAACAGAAAGAA 366
DB 307 TTGATTTACAAAAGAAAGATGATGATTTGGTCACCTATATCTTAAAGAAACAGAAAGAA 366
QY 367 TCCAAAATTAAGATCTTTCTGAAATGTGAGGCCAAAGATTTATCTGACGTTTCACATGC 426
DB 367 TCCAAAATTAAGATCTTTCTGAAATGTGAGGCCAAAGATTTATCTGACGTTTCACATGC 426
QY 427 TGTGGCGTGAAGGCAATCAGTACGATTTGAAATTCAGTGCACAAAGTACGAGGCGTTC 486
DB 427 TGTGGCGTGAAGGCAATCAGTACGATTTGAAATTCAGTGCACAAAGTACGAGGCGTTC 486
QY 487 TCTGACCCCAAGGCGTGACATGTGAGCAGTGAACCTTTTCAGCAGAGAGGCTCAGAGTG 546
DB 487 TCTGACCCCAAGGCGTGACATGTGAGCAGTGAACCTTTTCAGCAGAGAGGCTCAGAGTG 546
QY 547 GACAACAGGATTTTAAGAACTACACAGTGTGATGACAGAGGCGAGTGCCTGCCCTCT 606
DB 547 GACAACAGGATTTTAAGAACTACACAGTGTGATGACAGAGGCGAGTGCCTGCCCTCT 606
QY 607 GCCGAGGAGGCTTACCAGTGAAGTGTGATGATTCACAAAGTCAAGTATGAA 666
DB 607 GCCGAGGAGGCTTACCAGTGAAGTGTGATGATTCACAAAGTCAAGTATGAA 666
QY 667 AACTACACAGCAGCTTCTTCATCAGAGACATCATCAAAACAGCCAGCCAAACCTG 726
DB 667 AACTACACAGCAGCTTCTTCATCAGAGACATCATCAAAACAGCCAGCCAAACCTG 726
QY 727 CAGCTGAAGCATTGAAAATTTCTGGCAGCTGAGAGTCAAGTGGAAATACCCGACACC 786
DB 727 CAGCTGAAGCATTGAAAATTTCTGGCAGCTGAGAGTCAAGTGGAAATACCCGACACC 786
QY 787 TGGAGACACCCCAATCTCTACTTCTCCCTGACATTTTGCATACAGGCCAGGCAAGAAC 846
DB 787 TGGAGACACCCCAATCTCTACTTCTCCCTGACATTTTGCATACAGGCCAGGCAAGAAC 846
QY 847 AATAGAGAAAAGAAAGATAGACTCTGCTGACAAAGACCTTCAGCCAAAGTCTGTCAC 906
DB 847 AATAGAGAAAAGAAAGATAGACTCTGCTGACAAAGACCTTCAGCCAAAGTCTGTCAC 906
QY 907 AAGATGCGCAAGATCCCGCTGCAAGCCGAGAGCCGCTACTATATCTTATCTGAGGAC 966
DB 907 AAGATGCGCAAGATCCCGCTGCAAGCCGAGAGCCGCTACTATATCTTATCTGAGGAC 966
QY 967 TGGCATCTGTGTC 980
DB 967 TGGCATCTGTGTC 980
RESULT 4
AAI64388
ID AAI64388 standard: DNA: 990 BP.
XX
XX AAI64388:
AC
XX
XX 23-NOV-2001 (first entry)
DT
XX
DE Canine coding sequence #3.
XX
XX Canine: dog; immunostimulant; Interleukin 12; IL12; immunopathy; ds.
```

```

XX  Canis familiaris.
OS
XX
FH  Key      Location/Qualifiers
FT  CDS      1..990
FT          /*tag= a
FT          /product= "Canine protein #1"
FT  sig_peptide  1..65
FT          /*tag= b
FT  mat_peptide  67..987
FT          /*tag= c
XX
XX  JP2001161378-A.
XX
XX  19-JUN-2001.
XX
XX  26-SEP-2000: 2000JP-029294b.
XX
XX  01-OCT-1999: 95JP-0281234.
XX
XX  (TORA ) TORAY IND INC.
XX
XX  WPI: 2001-592466/67.
XX
XX  P-PSDB: AAG56482.
XX
XX  Preparation of a highly pure protein, interleukin 12, a protein
XX  inhibiting the activity of interleukin 12, and a treating agent and a
XX  treating method for immunopathy of mammalian
XX
XX  Claim 6: Page 16-17; 21pp; Japanese.
XX
XX  The present invention relates to a method for the preparation of a highly
XX  pure protein in which interleukin 12 (IL12) and/or a protein inhibiting
XX  the activity of IL12 is connected to an ion exchanging carrier and/or a
XX  pigment carrier to get IL12 and/or a protein inhibiting the activity of
XX  IL12. The protein is used as a preventive agent for dog immunopathy. The
XX  present sequence was used in the method of the present invention.
XX
XX  Sequence 990 BP: 275 A; 244 C; 245 G; 218 T; 0 other:
XX
Query Match      60.9%; Score 974; DB 22; Length 990;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 974; Conservative 0; Mismatches 0; Indels 0; Gaps 0:

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DB  427  TGGTGCGCTGACGGCATCTACTGATTTGGAATTTAGTGTCAAAGTAGCAGAGGCTTC 486
      |||||||
QY  487  TCTGACCCCCAMAGGGGTGACATGTGAGAGCTGACACTTTCCAGCAGAGAGGTCAGAGTG 546
      |||||||
DB  487  TCTGACCCCCAMAGGGGTGACATGTGAGAGCTGACACTTTCCAGCAGAGAGGTCAGAGTG 546
      |||||||
QY  547  GACAAACGGGATTTAAGAAGTACACAGTGTGATGTCAGAGAGGCGAGTGTGCCCCCTCT 606
      |||||||
DB  547  GACAAACGGGATTTAAGAAGTACACAGTGTGATGTCAGAGAGGCGAGTGTGCCCCCTCT 606
      |||||||
QY  607  GCCGAGAGAGCCCTACCCATCGAGGTCTGTGGATGCTATTTCAGCAAGCTCAAGTATGAA 666
      |||||||
DB  607  GCCGAGAGAGCCCTACCCATCGAGGTCTGTGGATGCTATTTCAGCAAGCTCAAGTATGAA 666
      |||||||
QY  667  AACTACAGCAGCAGCTTCTTCATCAGAGACATCATCAAAACAGAGCCACCAACCTTG 726
      |||||||
DB  667  AACTACAGCAGCAGCTTCTTCATCAGAGACATCATCAAAACAGAGCCACCAACCTTG 726
      |||||||
QY  727  CAGCTGACCCATTTGAAAAATTTCTGGCAGCTGTGAGGTGAGGGAATATCCCGACACC 786
      |||||||
DB  727  CAGCTGACCCATTTGAAAAATTTCTGGCAGCTGTGAGGTGAGGGAATATCCCGACACC 786
      |||||||
QY  787  TGGAGCAGCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCAGGCGAAGAC 846
      |||||||
DB  787  TGGAGCAGCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCAGGCGAAGAC 846
      |||||||
QY  847  AATGAGAAAGAAAGATAGACTCTGCTGACAGAGACCTCAGCCAGGTCGTGCCAC 906
      |||||||
DB  847  AATGAGAAAGAAAGATAGACTCTGCTGACAGAGACCTCAGCCAGGTCGTGCCAC 906
      |||||||
QY  907  AAGATGCCCAAGATTCGCCGTGCCAAGCCGAGACCGCTACTATGATTCATCTGTGAGCGAC 966
      |||||||
DB  907  AAGATGCCCAAGATTCGCCGTGCCAAGCCGAGACCGCTACTATGATTCATCTGTGAGCGAC 966
      |||||||
QY  967  TGGGCACTCTGTGTC 980
      |||||||
DB  967  TGGGCACTCTGTGTC 980
      |||||||

RESULT 5
AAVI3816
ID  AAVI3816 standard; cDNA to mRNA; 990 BP.
XX
AC  AAVI3816;
XX
DT  14-MAY-1998 (first entry)
XX
DE  Canine IL-12 p40 subunit cDNA.
XX
KW  Canine; interleukin-12 p40 subunit; IL-12 p40 subunit; antitumour;
XX  antiviral; vaccine adjuvant; ds.
XX
OS  Canis sp.
XX
FH  Key      Location/Qualifiers
FT  CDS      1..990
FT          /*tag= a
FT          /product= interleukin-12_p40_subunit
XX
XX  JP10036397-A.
XX
XX  10-FEB-1998.
XX
XX  08-NOV-1996: 95JP-0296789.
XX
XX  23-MAY-1996: 96JP-0128104.
XX
XX  08-NOV-1995: 95JP-0289729.
XX
XX  (TORA ) TORAY IND INC.
XX
XX  WPI: 1998-174514/16.
XX
XX  P-PSDB: AAM41750.

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XX Canine interleukin 12 - comprises P40 and p35 subunits; useful in
PT veterinary medicine, e.g. antitumour, antiviral and vaccine adjuvant
PT activities are expected

PS Claim 8; Page 8; 12pp; Japanese.

XX The present sequence encodes a canine interleukin-12 (IL-12) P40
CC subunit. A canine IL-12 comprising a P40 and p35 subunit is capable
CC of inducing an antiviral activating factor and the expression of
CC class II MHC molecules in canine tumour cells, stimulating
CC proliferation of canine blastogenic lymphocytes and activating
CC canine leukocytes to inhibit canine tumour cells. The canine IL-12
CC can be used in veterinary medicines, e.g. antitumour, antiviral and
CC vaccine adjuvant activities are expected.

XX Sequence 990 BP; 278 A; 243 C; 251 G; 218 T; 0 other;

Query Match 56.3%; Score 900; DB 19; Length 990;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 950; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

OY 28 TGGTTTCCCTGCTTTGCTGCGCTCTCCCTCATGCGCATATGGGAAGTGAAGAAGT 87
DB 28 TGGTTTCCCTGCTTTGCTGCGCTCTCCCTCATGCGCATATGGGAAGTGAAGAAGT 87
OY 88 GTTATGTTGATGAGTGGAGTGGACCGCTGATGCCCGGAGAAATGGTGTCTCCACCC 147
DB 88 GTTATGTTGATGAGTGGAGTGGACCGCTGATGCCCGGAGAAATGGTGTCTCTCACCC 147
OY 148 TGGCATACCCCTGGAAGAAGATGACATCATCTGGACCTCAGCGCAGAGCAGTGAAGTCTTA 207
DB 148 TGGCATACCCCTGGAAGAAGATGACATCATCTGGACCTCAGCGCAGAGCAGTGAAGTCTTA 207
OY 208 GGTCTGTGAAACGTCATGACCATCCAGTCAAGAAATTTGGAGATGCTGGCCAGATATACC 267
DB 208 GGTCTGTGAAACGTCATGACCATCCAGTCAAGAAATTTGGAGATGCTGGCCAGATATACC 267
OY 268 TGGCATAAGAGAGGAGGAGTTCAGCGCTCCTGTTGATTCACAAAAAAGAAAGAT 327
DB 268 TGGCATAAGAGAGGAGGAGTTCAGCGCTCCTGTTGATTCACAAAAAAGAAAGAT 327
OY 328 GGAATTTGGTCCACTGATATCTTAAAGAACAGAAAGAAATCCAAATTAAGATCTTTCTG 387
DB 328 GGAATTTGGTCCACTGATATCTTAAAGAACAGAAAGAAATCCAAATTAAGATCTTTCTG 387
OY 388 AAATGTGAGGCAAAAGATTAATCTGAGGTTTCACATGCTGGTGGCTACGGCAGATTCAGT 447
DB 388 AAATGTGAGGCAAAAGATTAATCTGAGGTTTCACATGCTGGTGGCTACGGCAGATTCAGT 447
OY 448 ACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTCTGAGCCCAAGGGGTGACA 507
DB 448 ACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTCTGAGCCCAAGGGGTGACA 507
OY 508 TGTGAGAGCAGTACACTTTTACAGAGAGGCTCAGAGTGGACACAGGATTTATAGAAG 567
DB 508 TGTGAGAGCAGTACACTTTTACAGAGAGGCTCAGAGTGGACACAGGATTTATAGAAG 567
OY 568 TACACAGTGGAGTGTGAGAGAGGCGAGTGGCTGCTGGCCGAGAGAGGCTTACCCATC 627
DB 568 TACACAGTGGAGTGTGAGAGAGGCGAGTGGCTGCTGGCCGAGAGAGGCTTACCCATC 627
OY 628 GAGGTGCTGTGATGATATTTCACAAAGCTCAAGTATGAAAATACACAGCAGCTTCTTC 687
DB 628 GAGGTGCTGTGATGATATTTCACAAAGCTCAAGTATGAAAATACACAGCAGCTTCTTC 687
OY 688 ATCAGAGACATATCAAAACAGACCCACCAAAACCTGACAGCTGAAGCATTTGAATAAT 747
DB 688 ATCAGAGACATATCAAAACAGACCCACCAAAACCTGACAGCTGAAGCATTTGAATAAT 747
OY 748 TCTCGGACGCTGGAGTGAAGTGGGAATATCCCGGACACTGGAGACACCCACATTCCTAC 807
DB 748 TCTCGGACGCTGGAGTGAAGTGGGAATATCCCGGACACTGGAGACACCCACATTCCTAC 807

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OY 808 TTCTCCCTGACATTTTGGATACAGGCCAGGCAAGAACATAGAGAAAAGAAATAGA 867
DB 808 TTCTCCCTGACATTTTGGATACAGGCCAGGCAAGAACATAGAGAAAAGAAATAGA 867
OY 868 CTCTCGTGGACAGACCTCAGCCCAAGGTGCTGTGCCACAGAGATGCCAAGATCCGCGTG 927
DB 868 CTCTCGTGGACAGACCTCAGCCCAAGGTGCTGTGCCACAGAGATGCCAAGATCCGCGTG 927
OY 928 CAAGCCCGAGACCGCTACTATGATTCATCTCTGAGCAGCTGGCATCTGTG 978
DB 928 CAAGCCCGAGACCGCTACTATGATTCATCTCTGAGCAGCTGGCATCTGTG 978

```

RESULT 6

AAK35615

ID AAK35615 standard: cDNA to mRNA; 990 BP.

AC AAK35615;

DT 09-JUL-1999 (first entry)

DE Nucleic acid encoding canine Interleukin-12 (IL-12).

KW Interleukin-12; IL-12; dog; cat; immune disease; Cani12; heterodimer;

KW tumour; skin disease; infectious disease; allergic disease; ds.

OS Canis sp.

PH Key Location/Qualifiers

FT CDS 1..990

FT /*tag= a

PN JP11106350-A.

PD 20-APR-1999.

PF 15-MAY-1998; 98JP-0133345.

PR 07-AUG-1997; 97JP-0213755.

PR 16-MAY-1997; 97JP-0127690.

XX (TORA) TORAY IND INC.

XX WPI; 1999-308068/26.

DR P-PSDB: AAY02339.

PT A prevention and treating agent containing interleukin 12 (Cani12) -

PT for prevention and treatment of dog and cat immune diseases

PS Claim 1; Page 12; 16pp; Japanese.

XX The present sequence encodes canine interleukin-12 (IL-12). The
CC specification describes a method for the prevention and treatment
CC of dog and cat immune diseases. The treatment used an agent comprising
CC dog IL-12 (Cani12) proteins to form a heterodimer. The agent is
CC useful for preventing and treating dog and cat immune diseases,
CC including tumours, skin diseases, infectious diseases and allergic
CC diseases.

XX Sequence 990 BP; 278 A; 243 C; 251 G; 218 T; 0 other;

Query Match 56.3%; Score 900; DB 20; Length 990;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 950; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

OY 28 TGGTTTCCCTGCTTTGCTGCGCTCTCCCTCATGCGCATATGGGAAGTGAAGAAGT 87
DB 28 TGGTTTCCCTGCTTTGCTGCGCTCTCCCTCATGCGCATATGGGAAGTGAAGAAGT 87
OY 88 GTTATGTTGATGAGTGGAGTGGACCGCTGATGCCCGGAGAAATGGTGTCTCTCACCC 147
DB 88 GTTATGTTGATGAGTGGAGTGGACCGCTGATGCCCGGAGAAATGGTGTCTCTCACCC 147

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148 TCCCATATCCCTGAAGAAATGACATCACTTGGACCTTCAGCCGACAGCAGTAGTCTTA
148 TGGCATATGCCCTGAGAAAGATGACATCACTTGGACCTTCAGCCGACAGCAGTAGTCTTA
208 GGTTCCTGATTAAGACTGTGACATCCAAAGATTTGGAGATGCTGGCCAGTATACC
208 GCTTCCTGATTAAGACTGTGACATCCAAAGATTTGGAGATGCTGGCCAGTATACC
268 TCCCATTAAGAGAGCAGCTTCTGAGCCGCTCAGCTCTCTTATTTCACAAAAAGAGAT
268 TCCCATTAAGAGAGCAGCTTCTGAGCCGCTCAGCTCTCTTATTTCACAAAAAGAGAT
328 GGAATTTGGTCCACTGATATCTTAAAGAGCAAAAGATTCAAAAATTAAGATCTTCTG
328 GGAATTTGGTCCACTGATATCTTAAAGAGCAAAAGATTCAAAAATTAAGATCTTCTG
388 AATGCTGAAGCAAGCAATTTCTGTGACCTTTCAGCTTTCAGCTGCTGAGCCGATCACT
388 AATGCTGAAGCAAGCAATTTCTGTGACCTTTCAGCTTTCAGCTGCTGAGCCGATCACT
448 ACTGATTTGAATTTAGTGTCAAAAGTACGAGAGGCTTCTGTGACCCCAAGCGGTGACA
448 ACTGATTTGAATTTAGTGTCAAAAGTACGAGAGGCTTCTGTGACCCCAAGCGGTGACA
508 TGTGGAGTACGACACTTTCAGCAGAGAGGCTCAGAGTGCAGACACAGGCAATTAAGAG
508 TGTGGAGTACGACACTTTCAGCAGAGAGGCTCAGAGTGCAGACACAGGCAATTAAGAG
568 TACACAGTGGAGTGTTCAGAGAGGCACTGCCCTCTGCCAGAGAGAGCCCTACCCATC
568 TACACAGTGGAGTGTTCAGAGAGGCACTGCCCTCTGCCAGAGAGAGCCCTACCCATC
628 GAGGTCTGTGTGATGCTATTCACAAAGCTCAAGTATGAAGACTACACCGACGCTTCTTC
628 GAGGTCTGTGTGATGCTATTCACAAAGCTCAAGTATGAAGACTACACCGACGCTTCTTC
688 ATCAGACAGCATCATCAAAATCAGACCGACCCAGCAAGCTCAGCTGAAGCTTTGAAAAAT
688 ATCAGACAGCATCATCAAAATCAGACCGACCCAGCAAGCTCAGCTGAAGCTTTGAAAAAT
748 TCTGGGCACTGTGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA
748 TCTGGGCACTGTGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA
808 TTTCTGCTGACATTTTGTATACAGGCCCAAGGCCAAGAAATAGAGAAAGATAGAGA
808 TTTCTGCTGACATTTTGTATACAGGCCCAAGGCCAAGAAATAGAGAAAGATAGAGA
868 CTCTGCTGAGACAGACCTTCAGCCAAAGCTGTGTGCTCAGCAAGATGCGCAAGTCCGCTG
868 CTCTGCTGAGACAGACCTTCAGCCAAAGCTGTGTGCTCAGCAAGATGCGCAAGTCCGCTG
928 CAAAGCCCAAGACCGCTACTATATAGTTTCATCTCTGAGCGAGCTGGGCAATCTGTG
928 CAAAGCCCAAGACCGCTACTATATAGTTTCATCTCTGAGCGAGCTGGGCAATCTGTG
928 CAAAGCCCAAGACCGCTACTATATAGTTTCATCTCTGAGCGAGCTGGGCAATCTGTG

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KW allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
KW dog Parvovirus infection; distemper virus; cat plaque virus infection;
KW feline leukemia; allergy; pollinosis; ds.
XX
OS Canis sp.
XX
Key Location/Qualifiers
XX CDS 1..990
XX /tag= a
XX /product= interleukin_12
XX
W09851327-A1.
XX
19-NOV-1998.
XX
07-MAY-1998: 98W0-JP02031.
XX
16-MAY-1997: 97JP-0127690.
XX
(TOKA ) TOKAY IND INC.
XX
Okano F, Satoh M, Yamada K:
XX
WPI: 1999-070100/06.
XX
P-PSDB: AAWB4371.
XX
New therapeutic and prophylactic agents - comprise
XX genetically-engineered canine interleukin 12, used to treat, e.g.
XX canine and feline immunological diseases
XX
Claim 1: Page 23-25; 45pp; Japanese.
XX
The present sequence encodes a canine interleukin 12 (IL-12) protein.
XX The IL-12 protein can be used in therapeutic or prophylactic agents.
XX The agents can be used to prevent and treat canine and feline
XX immunological diseases including dog and cat tumours, skin diseases,
XX viral infections and allergic diseases, especially tumours, breast
XX tumour, oesinophilic granuloma, epidermoid tumour, skin tumour, lipoma,
XX othematoma, pneumonodema, skin soft pedicled soft tumour and anal
XX tumour; skin diseases, otitis externa, dermatitis, eczema, fungal
XX traumatic dermatitis and hair loss; infections; dog parvovirus infection
XX and distemper virus, cat plaque virus infection and feline leukemia, and
XX allergic diseases, e.g. pollinosis.
XX
Sequence 990 BP: 278 A; 243 C; 251 G; 218 T; 0 other:
XX
Query Match 56.3%; Score 900; DB 20; Length 990;
XX Best Local Similarity 99.5%; Pred. No. 0;
XX Matches 950; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 28 TGGTTTTCCCTGCTGCTGCGCTCCCTCATGCGCATATGGGAAGTGAAGAT 87
DB 28 TGGTTTTCCCTGCTGCTGCGCTCCCTCATGCGCATATGGGAAGTGAAGAT 87
QY 88 GTTTATGTTGTAGAGTTGAGTGGACCTGATGACCTGATGACCTGATGACCTGATGACCT
DB 88 GTTTATGTTGTAGAGTTGAGTGGACCTGATGACCTGATGACCTGATGACCTGATGACCT
147
QY 148 TCCCATATCCCTGAAGAAATGACATCACTTGGACCTTCAGCCGACAGCAGTAGTCTTA
DB 148 TGGCATATGCCCTGAGAAAGATGACATCACTTGGACCTTCAGCCGACAGCAGTAGTCTTA
207
QY 208 GGTTCCTGATTAAGACTGTGACATCCAAAGATTTGGAGATGCTGGCCAGTATACC
DB 208 GGTTCCTGATTAAGACTGTGACATCCAAAGATTTGGAGATGCTGGCCAGTATACC
267
QY 268 TCCCATTAAGAGAGCAGCTTCTGAGCCGCTCAGCTCTCTTATTTCACAAAAAGAGAT
DB 268 TCCCATTAAGAGAGCAGCTTCTGAGCCGCTCAGCTCTCTTATTTCACAAAAAGAGAT
327
QY 328 GGAATTTGGTCCACTGATATCTTAAAGAGCAAAAGATTCAAAAATTAAGATCTTCTG
DB 328 GGAATTTGGTCCACTGATATCTTAAAGAGCAAAAGATTCAAAAATTAAGATCTTCTG
387

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Db 328 GGAATTGGTCCACTGATATCTTAAAGAGACAGAAAGANTCCAAAATAAGATCTTTCTG 387
OY 388 AAATGTGAGCGCAAGAAATTATTCTGAGCTTTCACATGCTGTGGCTGACCGCAATCAGT 447
    |||||||
Db 388 AAATGTGAGCGCAAGAAATTATTCTGAGCTTTCACATGCTGTGGCTGACCGCAATCAGT 447
OY 448 ACTGATTTGAAATTCAGTGTCAAAAAGTAGCAGAGGCTTCTCTGACCCCAAGGGGTGACA 507
    |||||||
Db 448 ACTGATTTGAAATTCAGTGTCAAAAAGTAGCAGAGGCTTCTCTGACCCCAAGGGGTGACA 507
OY 508 TGTGAGGAGGAGACACTTTCAGCAGAGGGGTGAGAGGAGCAACAGGATTTATTAAGAG 567
    |||||||
Db 508 TGTGAGGAGGAGACACTTTCAGCAGAGGGGTGAGAGGAGCAACAGGATTTATTAAGAG 567
OY 568 TACACAGTGTGAGTGTCAAGAGGGCAGTGTGCTGCTGCGCGAGAGAGGCTTACCCATC 627
    |||||||
Db 568 TACACAGTGTGAGTGTCAAGAGGGCAGTGTGCTGCTGCGCGAGAGAGGCTTACCCATC 627
OY 628 GAGGTCTGTGATGTCTATTACACAGCTCAAGTATGAAACTACACAGGAGCTTCTTC 687
    |||||||
Db 628 GAGGTCTGTGATGTCTATTACACAGCTCAAGTATGAAACTACACAGGAGCTTCTTC 687
OY 688 ATCAGAGACATCATCAACACAGACCCACCCCAAAACCTGACAGCTGAACCATTTGAAAAAT 747
    |||||||
Db 688 ATCAGAGACATCATCAACACAGACCCACCCCAAAACCTGACAGCTGAAGCTTTGAAAAAT 747
OY 748 TCTGCGCAGCTGTGAGGTGAGGATATACCCGACACCTGAGAGCCCACTTCTCTAC 807
    |||||||
Db 748 TCTGCGCAGCTGTGAGGTGAGGATATACCCGACACCTGAGAGCCCACTTCTCTAC 807
OY 808 TTTCTCCCTGACATTTTGCATACAGGCCAGGCGCAAGAACATAGAGAAAGAGAGATAGA 867
    |||||||
Db 808 TTTCTCCCTGACATTTTGCATACAGGCCAGGCGCAAGAACATAGAGAAAGAGAGATAGA 867
OY 868 CTCTGCGGAGACAGACTCTACGCAAGGTGTGTGSCACAGAGATGCCAAGATCGGCTG 927
    |||||||
Db 868 CTCTGCGGAGACAGACTCTACGCAAGGTGTGTGSCACAGAGATGCCAAGATCGGCTG 927
OY 928 CAAGCCCGAGACCGCTACTATAGTTCAATCTGTGAGCGACTGGGCACTCTGTG 978
    |||||||
Db 928 CAAGCCCGAGACCGCTACTATAGTTCAATCTGTGAGCGACTGGGCACTCTGTG 978

RESULT 8
AAI64378
ID AAI64378 standard; DNA; 990 BP.
XX AAI64378:

23-NOV-2001 (first entry)
XX Canine coding sequence #1.
DE
XX
XX Canine; dog; immunostimulant; interleukin 12; IL12; immunopathy; ds.
KM
XX
XX Canis familiaris.
OS
XX
XX Key Location/Qualifiers
FH 1..990
FT CDS /*tag= a
FT sig_peptide 1..66
FT /*tag= b
FT mat_peptide 67..987
FT /*tag= c
XX
XX JP2001161378-A.
XX
XX 19-JUN-2001.
XX
XX 26-SEP-2000; 2000JP-0292946.
XX
XX 01-OCT-1999; 99JP-0281234.
```

```
XX
PA (TORA ) TORAY IND INC.
XX
DR WPI: 2001-592466/67.
DR P-PSDB: AAG66480.
XX
XX Preparation of a highly pure protein, interleukin 12, a protein
PT inhibiting the activity of interleukin 12, and a treating agent and a
PT treating method for immunopathy of mammalian
XX
PS Claim 6; Page 14; 21pp; Japanese.
XX
XX The present invention relates to a method for the preparation of a highly
CC pure protein in which interleukin 12 (IL12) and/or a protein inhibiting
CC the activity of IL12 is contacted to an ion exchanging carrier and/or a
CC pigment carrier to get IL12 and/or a protein inhibiting the activity of
CC IL12. The protein is used as a preventive agent for dog immunopathy. The
CC present sequence was used in the method of the present invention.
XX
SQ Sequence 990 BP; 278 A; 243 C; 251 G; 218 T; 0 other;
```

Query Match 56.3%; Score 900; DB 22; Length 990;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 950; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
OY 28 TGGTTTTCCCTCGTTTGTGCTGGCGCTTCCTCCATGCGCATATGGAACCTGGAGAAAGAT 87
    |||||||
Db 28 TGGTTTTCCCTCGTTTGTGCTGGCGCTTCCTCCATGCGCATATGGAACCTGGAGAAAGAT 87
OY 88 GTTTATGTGTAGAGCTTGAGCTGCACCCCTGTATGCCCCGAGAAATGTGTCTCACC 147
    |||||||
Db 88 GTTTATGTGTAGAGCTTGAGCTGCACCCCTGTATGCCCCGAGAAATGTGTCTCACC 147
OY 148 TGGCATACCCCTCGAAGAAAGATGACATCATCTGAGCTCAGAGCGCAGAGCTGAAGTCTTA 207
    |||||||
Db 148 TGGCATACCCCTCGAAGAAAGATGACATCATCTGAGCTCAGAGCGCAGAGCTGAAGTCTTA 207
OY 208 GGTTCCTGTAACCTCTGACCATCAAGTCAAAAGATTTTGAGATGCTGGCCAGTATACC 267
    |||||||
Db 208 GGTTCCTGTAACCTCTGACCATCAAGTCAAAAGATTTTGAGATGCTGGCCAGTATACC 267
OY 268 TGGCATTAAGAGGAGGAGGCTGTGAGCGGCTCACTCCGTGTGATTCACAAAAAGAGAT 327
    |||||||
Db 268 TGGCATTAAGAGGAGGAGGCTGTGAGCGGCTCACTCCGTGTGATTCACAAAAAGAGAT 327
OY 328 GGAATTTGTGTCACCTGATATCTTAAAGAGACAGAAAGATCCAAAAATTAAGATCTTTCTG 387
    |||||||
Db 328 GGAATTTGTGTCACCTGATATCTTAAAGAGACAGAAAGATCCAAAAATTAAGATCTTTCTG 387
OY 388 AAATGTGAGCGCAAGAAATTATTCTGAGCTTTCACATGCTGTGGCTGACCGCAATCAGT 447
    |||||||
Db 388 AAATGTGAGCGCAAGAAATTATTCTGAGCTTTCACATGCTGTGGCTGACCGCAATCAGT 447
OY 448 ACTGATTTGAAATTCAGTGTCAAAAAGTAGCAGAGGCTTCTCTGACCCCAAGGGGTGACA 507
    |||||||
Db 448 ACTGATTTGAAATTCAGTGTCAAAAAGTAGCAGAGGCTTCTCTGACCCCAAGGGGTGACA 507
OY 508 TGTGAGGAGGAGACACTTTCAGCAGAGGGGTGAGAGGAGCAACAGGATTTATTAAGAG 567
    |||||||
Db 508 TGTGAGGAGGAGACACTTTCAGCAGAGGGGTGAGAGGAGCAACAGGATTTATTAAGAG 567
OY 568 TACACAGTGTGAGTGTCAAGAGGGGAGTGTGCTGCTGCGCGAGAGAGGCTTACCCATC 627
    |||||||
Db 568 TACACAGTGTGAGTGTCAAGAGGGGAGTGTGCTGCTGCGCGAGAGAGGCTTACCCATC 627
OY 628 GAGGTCTGTGATGTCTATTACACAGCTCAAGTATGAAACTACACAGGAGCTTCTTC 687
    |||||||
Db 628 GAGGTCTGTGATGTCTATTACACAGCTCAAGTATGAAACTACACAGGAGCTTCTTC 687
OY 688 ATCAGAGACATCATCAACACAGACCCACCCCAAAACCTGACAGCTGAAGCCATTTGAAAAAT 747
    |||||||
Db 688 ATCAGAGACATCATCAACACAGACCCACCCCAAAACCTGACAGCTGAAGCCATTTGAAAAAT 747
```


PT Canine cytokine protein which activates canine cytotoxic T
PT lymphocytes - is useful for treatment of viral and autoimmune
XX diseases in dogs

Claim 8; Page 30-31; 51pp; Japanese.

XX This sequence encodes the canine lymphocyte activation factor (CLAF) of
CC the invention. CLAF activates lymphocytes, especially canine cytotoxic
CC T cells. The protein contains a p35 and a p40 subunit. CLAF or antibodies
CC recognising it may be used in the treatment of viral diseases in dogs
CC (such as canine distemper, canine parvovirus and canine infectious
CC hepatitis). The antibodies may also be used in isolation of CLAF from
CC culture of the transformant host cells by affinity chromatography. The
CC p40 homodimer can be used for the treatment of autoimmune diseases in
CC dogs.

XX Sequence 2154 BP; 663 A; 448 C; 477 G; 566 T; 0 other:

Query Match 41.2%; Score 658; DB 20; Length 2154;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 658; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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323 AAGATGGAATTTGGTCCACTGATATCTTAAAGACAGAAAGATCCAAAATTAAGATCT 382
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
377 AAGATGGAATTTGGTCCACTGATATCTTAAAGACAGAAAGATCCAAAATTAAGATCT 436
QY 383 TTCTGAAATGTGAGCAAAAGAAATTTCTGACGTTTGCACATGCTGTGCTGACGCGAA 442
DB 437 TTCTGAAATGTGAGCAAAAGAAATTTCTGACGTTTGCACATGCTGTGCTGACGCGAA 496
QY 443 TCAGTACGATTTTGAATTTCACTGTCACAAAGTACGAGAGGCTTCTGTGACCCCAAGGG 502
DB 497 TCAGTACGATTTTGAATTTCACTGTCACAAAGTACGAGAGGCTTCTGTGACCCCAAGGG 556
QY 503 TGACATGTGAGCACTGACACTTTTGCAGAGAGAGGCTGACAGTGCACAAAGAGATTATA 562
DB 557 TGACATGTGAGCACTGACACTTTTGCAGAGAGAGGCTGACAGTGCACAAAGAGATTATA 616
QY 563 AGAAGTACACAGTGAAGTGTGACAGAGGCGAGTGCCTGCGCCCTGCGAGAGAGCCCTAC 622
DB 617 AGAAGTACACAGTGAAGTGTGACAGAGGCGAGTGCCTGCGCCCTGCGAGAGAGCCCTAC 676
QY 623 CCATCGAGGTGGTGGATGCTATTCACAGGCTCAACTATGAACACACACAGCAGCT 682
DB 677 CCATCGAGGTGGTGGATGCTATTCACAGGCTCAACTATGAACACACACAGCAGCT 736
QY 683 TCTTCATCAGAGACATCATCAAAACAGACCCACCAACCTGACGCTGAAGCATTGA 742
DB 737 TCTTCATCAGAGACATCATCAAAACAGACCCACCAACCTGACGCTGAAGCATTGA 796
QY 743 AAAATTTCTGCGACGTGAGAGTCACTGCGAATACCCCGACACCTGAGACACCCACATT 802
DB 797 AAAATTTCTGCGACGTGAGAGTCACTGCGAATACCCCGACACCTGAGACACCCACATT 856
QY 803 CCTACTTCTCCCTGACATTTTGCATACAGGCCCGAGCAAGCAATAGAGAAAAGAAAG 862
DB 857 CCTACTTCTCCCTGACATTTTGCATACAGGCCCGAGCAAGCAATAGAGAAAAGAAAG 916
QY 863 ATAGACTCTGCGTGGACAAAGACCTCAGCAAGGTCGTGCGACAAAGAGTCCAAAGATCC 922
DB 917 ATAGACTCTGCGTGGACAAAGACCTCAGCAAGGTCGTGCGACAAAGATCCAAAGATCC 976
QY 923 GCGTGCAGAGCCCGAGACCGCTACTATAGTTCATCTCGAGGAGCAGCTGGCCTATGTGTC 980
DB 977 GCGTGCAGAGCCCGAGACCGCTACTATAGTTCATCTCGAGGAGCAGCTGGCCTATGTGTC 1034
```

RESULT 11
AAK18179
ID AAK18179 standard; cdna: 591 BP.
XX
AC AAK18179;
XX

DT 07-MAY-1999 (first entry)
XX
DE Canine mature CLAF p35 subunit coding sequence.

XX CLAF; canine lymphocyte activation factor; p35 subunit; p40 subunit; dog;
KW viral disease; canine distemper; canine parvovirus; autoimmune disease;
KW canine infectious hepatitis; ds.

OS Canis sp.

PN W0985511-A1.

XX 10-DEC-1998.

XX 26-MAY-1998; 98WO-JP02295.

XX 03-JUN-1997; 97JP-0161936.

XX (KAGA) CHEMO-SERO-THERAPEUTIC RES INST.

XX Eda Y, Imanura T, Maeda H, Tokiyoshi S;

XX WPI: 1999-070260/06.

XX P-PSDB: AAW74325.

PT Canine cytokine protein which activates canine cytotoxic T
PT lymphocytes - is useful for treatment of viral and autoimmune
XX diseases in dogs

PS Claim 8; Page 34-35; 51pp; Japanese.

XX This sequence encodes the canine lymphocyte activation factor (CLAF) of
CC the invention. CLAF activates lymphocytes, especially canine cytotoxic
CC T cells. The protein contains a p35 and a p40 subunit. CLAF or antibodies
CC recognising it may be used in the treatment of viral diseases in dogs
CC (such as canine distemper, canine parvovirus and canine infectious
CC hepatitis). The antibodies may also be used in isolation of CLAF from
CC culture of the transformant host cells by affinity chromatography. The
CC p40 homodimer can be used for the treatment of autoimmune diseases in
CC dogs.

XX Sequence 591 BP; 173 A; 146 C; 127 G; 145 T; 0 other:

Query Match 30.9%; Score 494; DB 20; Length 591;
Best Local Similarity 100.0%; Pred. No. 1.9e-240;
Matches 494; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

1076 TGAGAGCGGTGAGAGACACGCTTTCAGAGGCCACAGCAACTTGAATTAATTCCTGCA 1135
DB 68 TGAGAGCGGTGAGAGACACGCTTTCAGAGGCCACAGCAACTTGAATTAATTCCTGCA 127
QY 1136 CTTCCGAAGAGATTGATCATGATATACCAAGAGTAAACAGCAGCAGTGGAGCCT 1195
DB 128 CTTCCGAAGAGATTGATCATGATATACCAAGAGTAAACAGCAGCAGTGGAGCCT 187
QY 1196 GCTTACACAGTGAATTAACATGAATGAGAGTGTCCCTGCGCTTCAGAGAGATCTTTGA 1255
DB 188 GCTTACACAGTGAATTAACATGAATGAGAGTGTCCCTGCGCTTCAGAGAGATCTTTGA 247
QY 1256 TAACTAACGGGAGTGTGCTGCGCTTTCGAAGGCGCTTTTATAGCGTCTGTGCTTA 1315
DB 248 TAACTAACGGGAGTGTGCTGCGCTTTCGAAGGCGCTTTTATAGCGTCTGTGCTTA 307
QY 1316 GCAGCATCTATGAGAGCTTGAAGATGTACAGGATGGAATTCAGGCGATGAAGCAAG 1375
DB 308 GCAGCATCTATGAGAGCTTGAAGATGTACAGGATGGAATTCAGGCGATGAAGCAAG 367
QY 1376 TTTTAAATGATCCCAAGAGCAGATCTTCTGATCAAAACATGCTGACAGCTATGATG 1435
DB 368 TTTTAAATGATCCCAAGAGCAGATCTTCTGATCAAAACATGCTGACAGCTATGATG 427
QY 1436 AGCTGTTACAGGCGCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCTCCCTTAAG 1495
DB 1436 AGCTGTTACAGGCGCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCTCCCTTAAG 1495
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Lh 428 AGCTGTACAGGCCCTGAATTTCACAGCTGTGCTGACAGAAATCTCCCTTGAAG 487
OY 1496 AGCCGAGTTTATATAAACAATCAAGCTCTGATCTCTTCAGCTTTCAGAAATTC 1555
Db 488 AGCCGAGTTTATATAAACAATCAAGCTCTGATCTCTTCATCTTTCAGAAATTC 547
OY 1556 GTGCGGTGACCATC 1569
Db 548 GTGCGGTGACCATC 561

RESULT 12
AAV13819
ID AAV13819 standard: cDNA to mRNA: 669 BP.
AC AAV13819:
XX
XX 14-MAY-1998 (first entry)
DT
XX Canine IL-12 p35 subunit cDNA.
XX
XX Canine: interleukin-12 p35 subunit; IL-12 p35 subunit; antitumour;
XX antilethal; vaccine adjuvant; ds.
XX
XX Canis sp.
XX
XX Key Location/Qualifiers
XX CDS 1..669 /*tag= a
XX /product= interleukin-12_p35_subunit
XX
XX JP10036397-A.
XX
XX 10-FEB-1998.
XX
XX 08-NOV-1996: 96JP-0295785.
XX
XX 23-MAY-1996: 96JP-0128104.
XX 08-NOV-1995: 95JP-0289729.
XX
XX (TORA ) TORAY IND INC.
XX WPI: 1998-174914/16.
XX P-PSDB: AAW41793.
XX
XX Canine interleukin 12 - comprises p40 and p35 subunits; useful in
XX veterinary medicine, e.g. antitumour, antiviral and vaccine adjuvant
XX activities are expected
XX
XX Claim 11: Pages 11-12: 12pp; Japanese.
XX
XX
XX The present sequence encodes a canine interleukin-12 (IL-12) p35
XX subunit. A canine IL-12 comprising a p40 and p35 subunit is capable
XX of inducing an antiviral activating factor and the expression of
XX class II MHC molecules in canine tumour cells, stimulating
XX proliferation of canine blastogenic lymphocytes and activating
XX canine leukocytes to inhibit canine tumour cells. The canine IL-12
XX can be used in veterinary medicines, e.g. antitumour, antiviral and
XX vaccine adjuvant activities are expected.
XX
XX Sequence 669 BP: 185 A; 177 C; 144 G; 163 T; 0 other:
XX
XX
XX Query Match 30.94: Score 494: DB 19: Length 669:
XX Best Local Similarity 100.0%: Pred. NO. 1.9e+240:
XX Matches 494: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
OY 1076 TGAGAGCGCTCAGCAGCAGCTTCAGAGCGCAGCAAACTCTGAATATATTCCTGCA 1135
Db 143 TGAGAGCGCTCAGCAGCAGCTTCAGAGCGCAGCAAACTCTGAATATATTCCTGCA 202
OY 1136 CTTCGGAAGAGATTGATCATAGATATCAGAAAGATAAACGACAGCTGAGGCTT 1195
Db 203 CTTCGGAAGAGATTGATCATAGATATCAGAAAGATAAACGACAGCTGAGGCTT 262

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OY 1196 GCCTTACCGTGAATTAACCATGATGAGAGTTCCTGGCTTCCAGAGAGATCTTTGA 1255
Db 263 GCCTTACCGTGAATTAACCATGATGAGAGTTCCTGGCTTCCAGAGAGATCTTTGA 322
OY 1256 TAACTAACGGAGATTGCGCTGCGCTCTGGAAAGGCTCTTTATGACGCTCTGCTTA 1315
Db 323 TAACTAACGGAGATTGCGCTGCGCTCTGGAAAGGCTCTTTATGACGCTCTGCTTA 382
OY 1316 GCAGCATCTATGAGACTTGAAGATGTACGAGATGGAATTCAGGCCATGACGAAAGC 1375
Db 383 GCAGCATCTATGAGACTTGAAGATGTACGAGATGGAATTCAGGCCATGACGAAAGC 442
OY 1376 TTTTAAATGATCCCAAGAGGAGATCTTTCGATCAAAACATGCTGACACTATTCGATG 1435
Db 443 TTTTAAATGATCCCAAGAGGAGATCTTTCGATCAAAACATGCTGACACTATTCGATG 502
OY 1436 AGCTGTACAGGCCCTGAATTTCAACAGTGTGACTGTGCTGACAGAAATCTCCCTTGAAG 1495
Db 503 AGCTGTACAGGCCCTGAATTTCAACAGTGTGACTGTGCTGACAGAAATCTCCCTTGAAG 562
OY 1496 AGCCGAGTTTATATAAACAATCAAGCTCTGATCTCTTCAGCTTTCAGAAATTC 1555
Db 563 AGCCGAGTTTATATAAACAATCAAGCTCTGATCTCTTCAGCTTTCAGAAATTC 622
OY 1556 GTGCGGTGACCATC 1569
Db 623 GTGCGGTGACCATC 636

RESULT 13
AAV35626
ID AAV35626 standard: cDNA to mRNA: 669 BP.
AC AAV35626:
XX
XX 09-JUL-1999 (first entry)
XX
XX Nucleic acid encoding canine Interleukin-12 (IL-12).
XX
XX Interleukin-12: IL-12; dog; cat; immune disease; CatIL12; heterodimer;
XX tumour; skin disease; infectious disease; allergic disease; ds.
XX
XX Canis sp.
XX
XX Key Location/Qualifiers
XX CDS 1..669 /*tag= a
XX
XX JP11106350-A.
XX
XX 20-APR-1999.
XX
XX 15-MAY-1998: 98JP-0133345.
XX
XX 07-AUG-1997: 97JP-0213755.
XX 16-MAY-1997: 97JP-0127690.
XX
XX (TORA ) TORAY IND INC.
XX
XX WPI: 1999-308068/26.
XX P-PSDB: AAV02343.
XX
XX A prevention and treating agent containing interleukin 12 (CatIL12) -
XX for prevention and treatment of dog and cat immune diseases
XX
XX Claim 1: Page 15-16: 16pp; Japanese.
XX
XX The present sequence encodes canine interleukin-12 (IL-12). The
XX specification describes a method for the prevention and treatment
XX of dog and cat immune diseases. The treatment used an agent comprising
XX dog IL-12 (CatIL12) proteins to form a heterodimer. The agent is
XX useful for preventing and treating dog and cat immune diseases.

```

CC including tumours, skin diseases, infectious diseases and allergic
CC diseases.
XX
XX
SQ Sequence 669 BP; 184 A; 177 C; 145 G; 163 T; 0 other;

Query Match 30.9%; Score 494; DB 20; Length 669;
Best Local Similarly 100.0%; Pred. No. 1.9e-240;
Matches 494; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1076 TGAGAGCCGTCAGACACGCTTCAGAGGCGCAGACAACCTCTGATATTTATTCCTGCA 1135
|||||
Db 143 TGAGAGCCGTCAGACACGCTTCAGAGGCGCAGACAACCTCTGATATTTATTCCTGCA 202
|||||
QY 1136 CTTCGGAAGAGATTGATCATGATATCACAAGAGATTAACAGCAGACAGTGGAGCCT 1195
|||||
Db 203 CTTCGGAAGAGATTGATCATGATATCACAAGAGATTAACAGCAGACAGTGGAGCCT 262
|||||
QY 1196 GCTTACCACCTGGAATTAAACCTGATGAGAGTTCCTGGCTTCAGAGAGATCTCTTGA 1255
|||||
263 GCTTACCACCTGGAATTAAACCTGATGAGAGTTCCTGGCTTCAGAGAGATCTCTTGA 322
|||||
1256 TAACTAACGGGAGTTGGCTGGCTCTGTGAAAGGCTCTTTATGACGCTCTGCTTGA 1315
|||||
Db 323 TAACTAACGGGAGTTGGCTGGCTCTGTGAAAGGCTCTTTATGACGCTCTGCTTGA 382
|||||
QY 1316 GCAGCATCTATGAGAGCTTGAAGATGTACAGATGGAATTCAAGCCATGAGCAAAAGC 1375
|||||
Db 383 GCAGCATCTATGAGAGCTTGAAGATGTACAGATGGAATTCAAGCCATGAGCAAAAGC 442
|||||
QY 1376 TTTTAAATGATCCCAAGAGGAGATCTTTGATGATCAAAACATCTGACAGCTATGATG 1435
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Db 443 TTTTAAATGATCCCAAGAGGAGATCTTTGATGATCAAAACATCTGACAGCTATGATG 502
|||||
QY 1436 AGCTGTTACAGGCGCTGATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTGAAG 1495
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Db 503 AGCTGTTACAGGCGCTGATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTGAAG 562
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QY 1496 AGCGGATTTTATTAATAAATCAAGCTCTGATATCTTTTATGATGCTTTTCAGAATTC 1555
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Db 563 AGCGGATTTTATTAATAAATCAAGCTCTGATATCTTTTATGATGCTTTTCAGAATTC 622
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QY 1556 GTGGGATGACCATC 1569
|||||
Db 623 GTGGGATGACCATC 636

RESULT 14

MAX03163
MAX03163 standard; cDNA to mRNA; 669 BP.

MAX03163;

30-MAR-1999 (first entry)

Nucleic acid encoding canine interleukin 12.

Canine; interleukin 12; IL-12; feline; immunological disease; tumour;
skin disease; viral infection; allergic disease; breast tumour;
oesinophilic granuloma; epidermoid tumour; skin tumour; lipoma;
ohematoma; pneumoedema; skin soft pedicled soft tumour; anal tumour;
otitis externa; dermatitis; eczema; fungal skin disease; pyoderma;
allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
dog Parvovirus infection; distemper virus; cat plaque virus infection;
feline Leukemia; allergy; pollinosis; ds.

Canis sp.

Key Location/Qualifiers

FT 1..669
CDS /*tag= a
/product= interleukin_12

PN MO9851327-A1.

XX
PD 19-NOV-1998.
XX
PF 07-MAY-1998; 98MO-JP02031.
XX
PR 16-MAY-1997; 97JP-0127690.
XX
PA (TORA) TORAY IND INC.
XX
PI Okano F, Satoh M, Yamada K;
XX
DR WPI; 1999-070100/06.
XX
DR P-PDB; AAW84374.
XX
PT New therapeutic and prophylactic agents - comprise
PT genetically-engineered canine interleukin 12, used to treat, e.g.
PT canine and feline immunological diseases

PS Claim 1; Page 33-34; 45pp; Japanese.

CC The present sequence encodes a canine interleukin 12 (IL-12) protein.
CC The IL-12 protein can be used in therapeutic or prophylactic agents.
CC The agents can be used to prevent and treat canine and feline
CC immunological diseases including dog and cat tumours, skin diseases,
CC viral infections and allergic diseases, especially tumours, breast
CC tumour, oesinophilic granuloma, epidermoid tumour, skin tumour, lipoma,
CC ohematoma, pneumoedema, skin soft pedicled soft tumour and anal
CC tumour; skin diseases, otitis externa, dermatitis, eczema, fungal
CC diseases of the skin, pyoderma, allergic dermatitis, nettle rash,
CC traumatic dermatitis and hair loss; infections; dog Parvovirus infection
CC and distemper virus, cat plaque virus infection and feline Leukemia, and
CC allergic diseases, e.g. pollinosis.

SQ Sequence 669 BP; 184 A; 177 C; 145 G; 163 T; 0 other;

Query Match 30.9%; Score 494; DB 20; Length 669;
Best Local Similarly 100.0%; Pred. No. 1.9e-240;
Matches 494; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1076 TGAGAGCCGTCAGACACGCTTCAGAGGCGCAGACAACCTCTGATATTTATTCCTGCA 1135
|||||
Db 143 TGAGAGCCGTCAGACACGCTTCAGAGGCGCAGACAACCTCTGATATTTATTCCTGCA 202
|||||
QY 1136 CTTCGGAAGAGATTGATCATGATATCACAAGAGATTAACAGCAGACAGTGGAGCCT 1195
|||||
Db 203 CTTCGGAAGAGATTGATCATGATATCACAAGAGATTAACAGCAGACAGTGGAGCCT 262
|||||
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QY 1316 GCAGCATCTATGAGAGCTTGAAGATGTACAGATGGAATTCAAGCCATGAGCAAAAGC 1375
|||||
Db 383 GCAGCATCTATGAGAGCTTGAAGATGTACAGATGGAATTCAAGCCATGAGCAAAAGC 442
|||||
QY 1376 TTTTAAATGATCCCAAGAGGAGATCTTTGATGATCAAAACATCTGACAGCTATGATG 1435
|||||
Db 443 TTTTAAATGATCCCAAGAGGAGATCTTTGATGATCAAAACATCTGACAGCTATGATG 502
|||||
QY 1436 AGCTGTTACAGGCGCTGATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTGAAG 1495
|||||
Db 503 AGCTGTTACAGGCGCTGATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTGAAG 562
|||||
QY 1496 AGCGGATTTTATTAATAAATCAAGCTCTGATATCTTTTATGATGCTTTTCAGAATTC 1555
|||||
Db 563 AGCGGATTTTATTAATAAATCAAGCTCTGATATCTTTTATGATGCTTTTCAGAATTC 622
|||||
QY 1556 GTGGGATGACCATC 1569
|||||

DB 623 GTGCGTGACCATC 636

RESULT 15
AA164385
10 AA164389 standard; DNA: 669 BP.
XX
AC AA164385;
XX
DT 23-NOV-2001 (first entry)
XX
DE Canine coding sequence #4.
XX
KW Canine; dog; immunostimulant; interleukin 12; IL12; immunopathy; ds.
OS Canis familiaris.
XX
FH Key location/qualifiers
FT CDS 1..569
TT /tag= a
FT sig_peptide 1..75
FT /product= "Canine protein #4"
FT mat_peptide 75..565
FT /tag= b
FT /tag= c
PN JP2001161378-A.
XX
PD 19-JUN-2001.
XX
PF 26-SEP-2000; 2000JP-0292946.
XX
PK 01-OCT-1995; 95JP-0281234.
XX
PA (TORA) TORAY IND INC.
XX
DR WPI: 2001-592456/67.
DR P-PSDB: AAG56483.
XX
PT Preparation of a highly pure protein, interleukin 12, a protein
PT inhibiting the activity of interleukin 12, and a treating agent and a
PT treating method for immunopathy of mammalian
XX
PS Claim 6; Page 18; 21pp; Japanese.
XX
CC The present invention relates to a method for the preparation of a highly
CC pure protein in which interleukin 12 (IL12) and/or a protein inhibiting
CC the activity of IL12 is contacted to an ion exchanging carrier and/or a
CC pigment carrier to get IL12 and/or a protein inhibiting the activity of
CC IL12. The protein is used as a preventive agent for dog immunopathy. The
CC present sequence was used in the method of the present invention.
XX
SO Sequence 669 BP; 184 A; 177 C; 145 G; 163 T; 0 other;

Query Match 30.9%; Score 494; DB 22; Length 669;
Best Local Similarity 100.0%; Pred. No. 1.9e-240;
Matches 494; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1076 TGAGAGCGCTGAGCAACGCTTTCAGAGGCTGAGACAAACTCTAGATTATATTCCTTGA 1135
|||||
DB 143 TGAGAGCGCTGAGCAACGCTTTCAGAGGCTGAGACAAACTCTAGATTATATTCCTTGA 202
|||||
QY 1136 CTTTCCGAGAGATTGATCATGAGATATGACCAAGCATAAACGACAGCTGAGAGGCT 1195
|||||
DB 203 CTTTCCGAGAGATTGATCATGAGATATGACCAAGCATAAACGACAGCTGAGAGGCT 262
|||||
QY 1196 GCTTACGACCTGAGATTGAGATGAGAGATTGCTGCTGCGAGAGATCTCTTGA 1255
|||||
DB 263 GCTTACGACCTGAGATTGAGATGAGAGATTGCTGCTGCGAGAGATCTCTTGA 322
|||||
QY 1256 TAACCTAACGAGAGTTGCTGCGCTCTGAGAAAGGCTCTTTATVAGCGGTCTGTGCTTA 1315
|||||
DB 323 TAACCTAACGAGAGTTGCTGCGCTCTGAGAAAGGCTCTTTATVAGCGGTCTGTGCTTA 382
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QY 1316 GCAGCATCTATGAGGACTTTGAAGATGTACACAGATGGAATTCAGGCCATGAACGCAAGC 1375
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DB 383 GCAGCATCTATGAGGACTTTGAAGATGTACACAGATGGAATTCAGGCCATGAACGCAAGC 442
|||||
QY 1376 TTTTATATGATGCCCAAGAGCGAGATCTTCTGATCAAAACATGCGTACAGCTATCGATG 1435
|||||
DB 443 TTTTATATGATGCCCAAGAGCGAGATCTTCTGATCAAAACATGCGTACAGCTATCGATG 502
|||||
QY 1436 AGCTGTATACAGGCCCTTGAATTTCAACAGTGTGATGCTGCGACAGAAATCCTCCCTTGAAG 1495
|||||
DB 503 AGCTGTATACAGGCCCTTGAATTTCAACAGTGTGATGCTGCGACAGAAATCCTCCCTTGAAG 562
|||||
QY 1496 AGCCGGATTTTATTAATAACTAAATCAACGCTCTGCATACTTCTTCATGCTTTCAGAAATTC 1555
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DB 563 AGCCGGATTTTATTAATAACTAAATCAACGCTCTGCATACTTCTTCATGCTTTCAGAAATTC 622
|||||
QY 1556 GTGCGGTGACCATC 1569
|||||
DB 623 GTGCGGTGACCATC 636

Search completed: January 21, 2003, 15:55:31
Job time : 277 secs



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OM nucleic - nucleic search, using sw model

Run on: January 21, 2003, 15:45:33 : Search time 56 Seconds
(without alignments)
8756.717 Million cell updates/sec

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Perfect score: 1599

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Scoring table:

CHLGO_NGC
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 15338381 residues

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Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	798	49.9	990	4	US-09-079-984A-1 Sequence 1, Appli
3	494	30.9	659	4	US-09-079-984A-12 Sequence 12, Appli
4	443	27.7	659	4	US-09-079-984A-2 Sequence 2, Appli
5	59	4.7	650	1	US-08-186-529-3 Sequence 3, Appli
6	59	4.7	660	1	US-08-640-386A-3 Sequence 3, Appli
7	59	4.7	721	2	US-08-184-009-199 Sequence 199, App
8	59	4.7	721	2	US-08-458-356-199 Sequence 199, App
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10	59	3.7	762	4	US-08-848-760B-21 Sequence 21, Appli
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991 14 0.9 238 5 PCT-US93-05794-32 Sequence 32, Appl
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993 14 0.9 254 4 US-09-328-111-785 Sequence 785, App
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996 14 0.9 289 1 US-08-592-126-124 Sequence 124, App
997 14 0.9 314 1 US-07-841-646-33 Sequence 33, Appl
998 14 0.9 314 1 US-08-147-023-33 Sequence 33, Appl
999 14 0.9 314 1 US-08-447-570-33 Sequence 33, Appl
1000 14 0.9 314 2 US-08-449-700-33 Sequence 33, Appl

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ALIGNMENTS

```

RESULT 1
US-09-079-984A-11
: Sequence 11, Application US/09079984A
: Patent No. 6231850
: GENERAL INFORMATION:
: APPLICANT: Okano, Fumiyoshi, Satoh, Masahiro.
: TITLE OF INVENTION: Canine Interleukin 12, a production method
: TITLE OF INVENTION: thereof, an immune disease treatment method and preventive
: NUMBER OF SEQUENCES: 16
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Miller & Christenbury Intellectual Property
: ADDRESSEE: Department of Schneider, Harrison, Segal and Lewis, LLP
: STREET: 1600 Market Street, 39th Floor
: CITY: Philadelphia
: STATE: PA
: COUNTRY: USA
: ZIP: 19103
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy Disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: WordPerfect 5.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/079, 984A
: FILING DATE: 15-MAY-1998
: ATTORNEY/AGENT INFORMATION:
: NAME: Austin R. Miller
: REGISTRATION NUMBER: 16,602
: REFERENCE/DOCKET NUMBER: 1051-98
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (215) 563-1810
: TELEFAX: (215) 568-6946
: INFORMATION FOR SEQ ID NO: 11:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 990 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA to mRNA
: ORIGINAL SOURCE:
: ORGANISM: Canis familiaris
: FEATURE:

```

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: NAME/REV: Canine IL12
: LOCATION: 1 to 987
: IDENTIFICATION METHOD: Similarity
US-09-079-984A-11
Query Match 60.9%; Score 974; DB 4; Length 990;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 974; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 667 AACCTACACACAGCTTTTATCAGAGACATCATCAAAACAGGAGGAGGAGGAGG 726
QY 727 CAGCTGAAGGCAATGAAATTTCTGGCAGCTGGAGGCTGAGGAGGAGGAGGAGG 786
Db 727 CAGCTGAAGGCAATGAAATTTCTGGCAGCTGGAGGCTGAGGAGGAGGAGGAGG 786
QY 787 TGGAGCACCCCAATCTCTACTTCTCCCTGACATTTTGCATACAGGAGGAGGAGG 846
Db 787 TGGAGCACCCCAATCTCTACTTCTCCCTGACATTTTGCATACAGGAGGAGGAGG 846
QY 847 AATAGAGAAAAGAAAGATAGACTGTGCTGAGCAAGACCTGAGCAAGGTGTGCTG 906
Db 847 AATAGAGAAAAGAAAGATAGACTGTGCTGAGCAAGACCTGAGCAAGGTGTGCTG 906
QY 907 AAGGATGCAAGATCCGGTGTGCAAGGCGGAGCGGAGCTACTATAGTCTATGAGG 966
Db 907 AAGGATGCAAGATCCGGTGTGCAAGGCGGAGCGGAGCTACTATAGTCTATGAGG 966

```

QY 567 TGGCATCTGTCTC 580
|||||
Db 567 TGGCATCTGTCTC 580

RESULT 2
US-09-079-984A-1
: Sequence 1, Application US/05079984A
: Patent No. 6231850
: GENERAL INFORMATION:
: APPLICANT: Okano, Fumiyoshi, Satoh, Masahiro,
: APPLICANT: Yamada, Katsushige
: TITLE OF INVENTION: Canine Interleukin 12, a production method
: TITLE OF INVENTION: thereof, an immune disease treatment method and preventive
: TITLE OF INVENTION: method using it.
: NUMBER OF SEQUENCES: 16
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Miller & Christenbury Intellectual Property
: ADDRESSEE: Department of Schnader, Harrison, Segal and Lewis, LLP
: STREET: 1600 Market Street, 39th Floor
: CITY: Philadelphia
: STATE: PA
: COUNTRY: USA
: ZIP: 19103
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy Disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: WordPerfect 5.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/05/079, 984A
: FILING DATE: 15-MAY-1998
: ATTORNEY/AGENT INFORMATION:
: NAME: Austin R. Miller
: REGISTRATION NUMBER: 16,602
: REFERENCE/PACKET NUMBER: 1051-98
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (215) 563-1810
: TELEFAX: (215) 568-6545
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 590 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA to mRNA
: ORIGINAL SOURCE:
: ORGANISM: Canis familiaris
: FEATURE:
: NAME/KEY: Canine IL12
: LOCATION: 1 to 587
: IDENTIFICATION METHOD: Similarity
: US-09-079-984A-1

Query Match 45.94: Score 798: DB 4: Length 590:
Best Local Similarity 59.74: Pred. No. 0:
Matches 548: Conservative 0: Mismatches 3: Indels 0: Gaps 0:

QY 28 TGGTTTCGCTGCTTTGCTGACGCTGCTCCCTGATGCGCAATAGGGAAGTGGGAAGAT 87
|||||
Db 28 TGGTTTCGCTGCTTTGCTGACGCTGCTCCCTGATGCGCAATAGGGAAGTGGGAAGAT 87

QY 88 GTTATATGTTTAGAGTTGGACCTGGACCGCTGATGCTGCGGAGAAATGCTGCTGCACG 147
|||||
Db 88 GTTATATGTTTAGAGTTGGACCTGGACCGCTGATGCTGCGGAGAAATGCTGCTGCACG 147

QY 148 TGGCATACCTCTGAAGAAGATACATCACTTGACCTCAGCGCAAGAGCAGTGAAGTCTTA 207
|||||
Db 148 TGGCATACCTCTGAAGAAGATACATCACTTGACCTCAGCGCAAGAGCAGTGAAGTCTTA 207

QY 208 GGTTCGTGTAAGACTGTGACCATCCAGTCAAGAAATTTGAGATGCTGCGCATATACG 267
|||||
Db 208 GGTTCGTGTAAGACTGTGACCATCCAGTCAAGAAATTTGAGATGCTGCGCATATACG 267

QY 268 TGGCATAAAGGAGGCAAGGTTCTGAGCGGCTCAGCTCCTGTTGATTACACAAAAGAAGAT 327
|||||
Db 268 TGGCATAAAGGAGGCAAGGTTCTGAGCGGCTCAGCTCCTGTTGATTACACAAAAGAAGAT 327

QY 328 GGAATTTGCTCCACATATCTTAAAGSAGCAGAAAGATCAAAATTAAGATCTTTCTG 387
|||||
Db 328 GGAATTTGCTCCACATATCTTAAAGSAGCAGAAAGATCAAAATTAAGATCTTTCTG 387

QY 388 AAATGTGAGCAAAAGAAATTTATTTGACAGTTTTCACATGCTGCTGAGCGCAATCAGT 447
|||||
Db 388 AAATGTGAGCAAAAGAAATTTATTTGACAGTTTTCACATGCTGCTGAGCGCAATCAGT 447

QY 448 ACTGATTTGAATTCAGTTCAGTCAAAAGTACAGAGGCTTCTGACCCCGCAAGGGTGTACA 507
|||||
Db 448 ACTGATTTGAATTCAGTTCAGTCAAAAGTACAGAGGCTTCTGACCCCGCAAGGGTGTACA 507

QY 508 TGTGAGCAGTGACACTTTTCAGCAGAGAGGTCAAGAGTGAGCAACAGAGATTTATAGAG 567
|||||
Db 508 TGTGAGCAGTGACACTTTTCAGCAGAGAGGTCAAGAGTGAGCAACAGAGATTTATAGAG 567

QY 568 TACACAGTGSAGTGTACAGAGGGCAGTGCCTGCCCTCTGCCAGAGAGACCTACCATC 627
|||||
Db 568 TACACAGTGSAGTGTACAGAGGGCAGTGCCTGCCCTCTGCCAGAGAGACCTACCATC 627

QY 628 GAGTGTGCTGAGATGCTATTCACAGAGTCAAGTATGAAGTACACAGCAGCTTCTTC 687
|||||
Db 628 GAGTGTGCTGAGATGCTATTCACAGAGTCAAGTATGAAGTACACAGCAGCTTCTTC 687

QY 688 ATCAGAGACATCATCAAAACAGACCCCAAAACCTGACGCTGAAGCCATTGGAAT 747
|||||
Db 688 ATCAGAGACATCATCAAAACAGACCCCAAAACCTGACGCTGAAGCCATTGGAAT 747

QY 748 TCTCGGACGTGAGAGTCAAGCTGGGAATACCCGACACCTGAGAGACCCCATTCCTAC 807
|||||
Db 748 TCTCGGACGTGAGAGTCAAGCTGGGAATACCCGACACCTGAGAGACCCCATTCCTAC 807

QY 808 TTTCTCCCTGACATTTTGGATACAGGCCGAGGCAAGCAATATAGGAAAGAAATATGA 867
|||||
Db 808 TTTCTCCCTGACATTTTGGATACAGGCCGAGGCAAGCAATATAGGAAAGAAATATGA 867

QY 868 CTCTGCTGACAAAGACCTCAAGCAGTGTGTGCTCCCAAGAGATGCCAAGATCCGCTG 927
|||||
Db 868 CTCTGCTGACAAAGACCTCAAGCAGTGTGTGCTCCCAAGAGATGCCAAGATCCGCTG 927

QY 928 CAAGCCGAGACCGCTACTATATGTTCAATCTGAGACCACTGGGCAATCTGTG 978
|||||
Db 928 CAAGCCGAGACCGCTACTATATGTTCAATCTGAGACCACTGGGCAATCTGTG 978

RESULT 3
US-09-079-984A-12
: Sequence 12, Application US/09079984A
: Patent No. 6231850
: GENERAL INFORMATION:
: APPLICANT: Okano, Fumiyoshi, Satoh, Masahiro,
: APPLICANT: Yamada, Katsushige
: TITLE OF INVENTION: Canine Interleukin 12, a production method
: TITLE OF INVENTION: thereof, an immune disease treatment method and preventive
: TITLE OF INVENTION: method using it.
: NUMBER OF SEQUENCES: 16
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Miller & Christenbury Intellectual Property
: ADDRESSEE: Department of Schnader, Harrison, Segal and Lewis, LLP
: STREET: 1600 Market Street, 39th Floor
: CITY: Philadelphia
: STATE: PA
: COUNTRY: USA
: ZIP: 19103
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy Disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS

Query Match	30.9%	Score	494	DB 4	Length	669	
Best Local Similarity	100.0%	Pred. No.	2.9e-235				
Matches	494	Conservative	0	Mismatches	0	Gaps	0

RESULT 4
US-09-079-984A-2

```

; GENERAL INFORMATION:
; APPLICANT: Okano, Fumiyoshi, Satoh, Massahiro,
;

```

Query Match	27.7%	DB 43	length	669					
Best Local Similarity	99.8%	Score No. 5.4e-210							
Matches	493	Conservative	0	Mismatches	1	Indels	0	Gaps	0

QY	1 076	TGAGAGCCGTCACCAACACGCTTCGACAAAGCCGACGAAACTCTACAATTATATTTCTCTGCA	11353
Db	143	TGAGAGCCGTCACCAACACGCTTCGACAAAGCCGACGAAACTCTACAATTATATTTCTCTGCA	202
QY	1136	CTTTCGAGAGATTGATCATGAAGATATCAAAAGGATTAACACGACGACGTGAGGCGCT	11959
Db	203	CTTTCGAGAGATTGATCATGAAGATATCAAAAGGATTAACACGACGACGTGAGGCGCT	262
QY	1196	GCTTACCACTGGAATTAACCATGAATGACAGATGGCTGGCTTCGACAGAGATCTCTTTGA	12555
Db	263	GCTTACCACTGGAATTAACCATGAATGACAGATGGCTGGCTTCGACAGAGATCTCTTTGA	322
QY	1256	TAACTAACGGGAGATTGCTTCGGCCCTCTGGAAAGGCGCTCTTTTATGACGGTCTGTGCTTTA	13151
Db	323	TAACTAACGGGAGATTGCTTCGGCCCTCTGGAAAGGCGCTCTTTTATGACGGTCTGTGCTTTA	382
QY	1316	GCAGCATTCTGTGAGGCACTTGAACATCTACCACATGGAATTCAAGGCGCATGAAACGAACG	13759
Db	383	GCAGCATTCTGTGAGGCACTTGAACATCTACCACATGGAATTCAAGGCGCATGAAACGAACG	442
QY	1376	TTTTTAATGATCTCCCAAGAGCGCAGATCTTCTGGATCAAAACATCGCTGACAGCTATATCGAT	14359
Db	443	TTTTTAATGATCTCCCAAGAGCGCAGATCTTCTGGATCAAAACATCGCTGACAGCTATATCGAT	502
QY	1436	AGCTGTTACAGGCGCTTGAATTTTCAACAGTGTGACTGTGCACAGAAATCTCTCTTGAAG	14959

Db 503 AACGTTGAGGGCCGGAATTCAAGTGTGCTGTGCGAGAAATCCCTTGAGG 562
QY 1496 ACCGCAATTTTATAAAGTAATCAAGCTCTGATCTTCAAGCTTTCAGATTC 1555
|||||
Db 563 ACCGCAATTTTATAAAGTAATCAAGCTCTGATCTTTCAGATTC 622
QY 1556 GTGCGATTACATC 1569
|||||
Db 623 GTGCGATTACATC 636
RESULT 5
US-08-186-529-3
: Sequence 3, Application US/08186529
: Patent No. 5573764
: GENERAL INFORMATION:
: APPLICANT: Sykes, Megan
: TITLE OF INVENTION: USE OF INTERLEUKIN-12 TO PREVENT
: TITLE OF INVENTION: GRAFT-VERSUS-HOST DISEASE
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genetics Institute, Inc., Legal Affairs
: STREET: 87 Cambridgepark Drive
: CITY: Cambridge
: STATE: MA
: COUNTRY: USA
: ZIP: 02140
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent in Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/186, 529
: FILING DATE:
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: McDaniels, Patricia A.
: REGISTRATION NUMBER: 33,194
: REFERENCE/DOCKET NUMBER: G1 5225
: TELEPHONE: 617-498-8401
: TELEFAX: 617-876-5851
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 660 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: ORIGINAL SOURCE:
: ORGANISM: Homo sapiens
: CELL TYPE: Lymphoblast
: CELL LINE: RPMI 8856
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..660
: US-08-186-529-3
Query Match 3.7%; Score 59; DB 1; Length 660;
Best Local Similarity 100.0%; Pred. No. 1.2e-19;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 1498 CCGCATTTTATAAAGTAATCAAGCTCTGATCTTTCAGATTCG 1556
|||||
Db 556 CCGCATTTTATAAAGTAATCAAGCTCTGATCTTTCAGATTCG 614

RESULT 6
US-08-640-386A-3
: Sequence 3, Application US/08640386A
: Patent No. 5756085

: GENERAL INFORMATION:
: APPLICANT: Sykes, Megan
: TITLE OF INVENTION: USE OF INTERLEUKIN-12 TO PREVENT
: TITLE OF INVENTION: GRAFT-VERSUS-HOST DISEASE
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genetics Institute, Inc., Legal Affairs
: STREET: 87 Cambridgepark Drive
: CITY: Cambridge
: STATE: MA
: COUNTRY: USA
: ZIP: 02140
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent in Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/640,386A
: FILING DATE:
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: Brown, Scott A.
: REGISTRATION NUMBER: 32,724
: REFERENCE/DOCKET NUMBER: G1 5225A
: TELEPHONE: 617-498-8224
: TELEFAX: 617-876-5851
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 660 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: ORIGINAL SOURCE:
: ORGANISM: Homo sapiens
: CELL TYPE: Lymphoblast
: CELL LINE: RPMI 8866
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..660
: US-08-640-386A-3
Query Match 3.7%; Score 59; DB 1; Length 660;
Best Local Similarity 100.0%; Pred. No. 1.2e-19;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1498 CCGCATTTTATAAAGTAATCAAGCTCTGATCTTTCAGATTCG 1556
|||||
Db 556 CCGCATTTTATAAAGTAATCAAGCTCTGATCTTTCAGATTCG 614

RESULT 7
US-08-184-009-199
: Sequence 199, Application US/08184009
: Patent No. 5833975
: GENERAL INFORMATION:
: APPLICANT: Paolelli, Enzo
: APPLICANT: Tartaglia, James
: APPLICANT: Cox, William I.
: TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
: NUMBER OF SEQUENCES: 217
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Curtiss, Morris & Safford
: STREET: 530 Fifth Avenue
: CITY: New York
: STATE: NY
: COUNTRY: USA
: ZIP: 10036
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/184,009
FILING DATE: 19-JAN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2530
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
TELEX: 425066CURTMS
INFORMATION FOR SEQ ID NO: 199:
SEQUENCE CHARACTERISTICS:
LENGTH: 721 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
08-184-009-199

Query Match 3.7%; Score 59; DB 2; Length 721;
Best Local Similarity 100.0%; Pred. No. 1.2e-19;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1498 CCGGATTTTATAAACAATAATCAAGCTGCGATCTTCTTCATGCTTTCAGAAATTCG 1556
Db 617 CCGGATTTTATAAACAATAATCAAGCTGCGATCTTCTTCATGCTTTCAGAAATTCG 675

RESULT 8
US-08-458-356-199
Sequence 199, Application US/08458356
Patent No. 5942235
GENERAL INFORMATION:
APPLICANT: Paoletti, Enzo
APPLICANT: Tartaglia, James
APPLICANT: Cox, William I.
TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
NUMBER OF SEQUENCES: 217
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtiss, Morris & Safford
STREET: 530 Fifth Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,356
FILING DATE: 02-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/184,009
FILING DATE: 19-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2530
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
TELEX: 425066CURTMS
INFORMATION FOR SEQ ID NO: 199:
SEQUENCE CHARACTERISTICS:
LENGTH: 721 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-458-356-199

Query Match 3.7%; Score 59; DB 2; Length 721;
Best Local Similarity 100.0%; Pred. No. 1.2e-19;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1498 CCGGATTTTATAAACAATAATCAAGCTGCGATCTTCTTCATGCTTTCAGAAATTCG 1556
Db 617 CCGGATTTTATAAACAATAATCAAGCTGCGATCTTCTTCATGCTTTCAGAAATTCG 675

RESULT 9
US-08-460-736-199
Sequence 199, Application US/08460736
Patent No. 6265189
GENERAL INFORMATION:
APPLICANT: Paoletti, Enzo
APPLICANT: Tartaglia, James
APPLICANT: Cox, William I.
TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
NUMBER OF SEQUENCES: 217
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtiss, Morris & Safford
STREET: 530 Fifth Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,736
FILING DATE: 02-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/184,009
FILING DATE: 19-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2530
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
TELEX: 425066CURTMS
INFORMATION FOR SEQ ID NO: 199:
SEQUENCE CHARACTERISTICS:
LENGTH: 721 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-460-736-199

Query Match 3.7%; Score 59; DB 4; Length 721;
Best Local Similarity 100.0%; Pred. No. 1.2e-19;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1498 CCGGATTTTATAAACAATAATCAAGCTGCGATCTTCTTCATGCTTTCAGAAATTCG 1556
Db 617 CCGGATTTTATAAACAATAATCAAGCTGCGATCTTCTTCATGCTTTCAGAAATTCG 675

RESULT 10
US-08-848-760B-21
Sequence 21, Application US/08848760B

TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: HOMO SAPIENS
FEATURE:
NAME/KEY: CDS
LOCATION: 102..863
US-08-684-687-3

Query Match 3.7%; Score 59; DB 2; Length 1316;
Best Local Similarity 100.0%; Pred. No. 1.2e-19;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1498 CCGGATTTTATATAAATAATCAAGCTCTGCATACCTTCTTCATGCTTTCAGAAATTCG 1556
DB 759 CCGGATTTTATATAAATAATCAAGCTCTGCATACCTTCTTCATGCTTTCAGAAATTCG 817

ULT 13
US-09-851-520-3

Sequence 3, Application US/09851520
Patent No. 6399379
GENERAL INFORMATION:
APPLICANT: Brenda F. Baker

APPLICANT: Susan M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P35 SUBUNIT EXPRESSION
FILE REFERENCE: RTS-0241
CURRENT APPLICATION NUMBER: US/09/851,520
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 88
SEQ ID NO 3

LENGTH: 1316
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (102)...(863)
US-09-851-520-3

Query Match 3.7%; Score 59; DB 4; Length 1316;
Best Local Similarity 100.0%; Pred. No. 1.2e-19;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1498 CCGGATTTTATATAAATAATCAAGCTCTGCATACCTTCTTCATGCTTTCAGAAATTCG 1556
759 CCGGATTTTATATAAATAATCAAGCTCTGCATACCTTCTTCATGCTTTCAGAAATTCG 817

RESULT 14
US-08-265-087-3
Sequence 3, Application US/08265087
Patent No. 5571515

GENERAL INFORMATION:
APPLICANT: Scott, Phillip
APPLICANT: Trinchieri, Giorgio
TITLE OF INVENTION: Compositions and Methods for Use of
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Center, PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/265,087
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/229,282
FILING DATE: 18-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST51AUSA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9206
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1364 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 101..859
US-08-265-087-3

Query Match 3.7%; Score 59; DB 1; Length 1364;
Best Local Similarity 100.0%; Pred. No. 1.2e-19;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1498 CCGGATTTTATATAAATAATCAAGCTCTGCATACCTTCTTCATGCTTTCAGAAATTCG 1556
DB 758 CCGGATTTTATATAAATAATCAAGCTCTGCATACCTTCTTCATGCTTTCAGAAATTCG 816

RESULT 15
US-08-621-493-3

Sequence 3, Application US/08621493
Patent No. 5723127
GENERAL INFORMATION:
APPLICANT: Scott, Phillip

APPLICANT: Trinchieri, Giorgio
TITLE OF INVENTION: Compositions and Methods for Use of
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Center, PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/621,493
FILING DATE: 25-MAR-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/265,087
FILING DATE: 17-JUN-1994
APPLICATION NUMBER: US 08/229,282
FILING DATE: 18-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST51AUSA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9206
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
: LENGTH: 164 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: unknown
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 101..859
US-08-621-453-3

Query Match 3.74; Score 59; DB 1; Length 1364;
Best local Similarity 100.0%; Pred. No. 1.2e-19;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1448 CCGCATTTTATTAACATAAATCAAGCTTCGCATACCTTCTTCATGCTTTCAGAAATCG 1556
|||||
Db 758 CCGCATTTTATTAACATAAATCAAGCTTCGCATACCTTCTTCATGCTTTCAGAAATCG 816

Search completed: January 21, 2003, 17:12:41
Job time : 54 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 21, 2003, 16:43:45 : Search time 68 Seconds
(without alignments)
10484.462 Million cell updates/sec

Title: US-09-917-265-61

Perfect score: 1599

Sequence: 1 atgacacctcagcatttgc.....tgcctacttgaactcttcc 1599

Scoring table:

Gapop 60.0, Gapext 60.0

Searched: 393868 seqs, 222934145 residues

Word size : 0

Total number of hits satisfying chosen parameters: 787736

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 1000 summaries

Database : published_Applications-NA.*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
5: /cgn2_6/ptodata/1/pubpna/PCTUS_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
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11: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
12: /cgn2_5/ptodata/1/pubpna/US60_NEW_PUB.seq.*
13: /cgn2_5/ptodata/1/pubpna/US60_NEW_PUB.seq.*
14: /cgn2_5/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Print No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1599	100.0	1599	US-09-917-265-61	Sequence 61, App1
2	1599	100.0	1599	US-09-917-265-63	Sequence 63, App1
3	1533	95.9	1533	US-09-917-265-66	Sequence 66, App1
4	1533	95.9	1533	US-09-917-265-68	Sequence 68, App1
5	987	61.7	987	US-09-917-265-58	Sequence 58, App1
6	987	61.7	987	US-09-917-265-60	Sequence 60, App1
7	974	60.9	2267	US-09-917-265-107	Sequence 107, App
8	974	60.9	2267	US-09-917-265-109	Sequence 109, App
9	914	57.2	921	US-09-917-265-52	Sequence 52, App1
10	914	57.2	921	US-09-917-265-54	Sequence 54, App1
11	494	30.9	591	US-09-917-265-49	Sequence 49, App1
12	494	30.9	591	US-09-917-265-45	Sequence 45, App1
13	494	30.9	666	US-09-917-265-46	Sequence 46, App1
14	494	30.9	666	US-09-917-265-48	Sequence 48, App1
15	494	30.9	1455	US-09-917-265-104	Sequence 104, App
16	494	30.9	1455	US-09-917-265-106	Sequence 106, App
17	81	5.1	561	US-09-917-265-101	Sequence 101, App
18	81	5.1	561	US-09-917-265-103	Sequence 103, App
19	81	5.1	591	US-09-917-265-35	Sequence 35, App1

C	20	81	5.1	591	10	US-09-917-265-37	Sequence 37, App1
C	21	81	5.1	591	12	US-10-079-616-9	Sequence 9, App1
C	22	81	5.1	666	10	US-09-917-265-32	Sequence 32, App1
C	23	81	5.1	666	10	US-09-917-265-34	Sequence 34, App1
C	24	81	5.1	1441	12	US-10-079-616-8	Sequence 8, App1
C	25	81	5.1	1533	10	US-09-917-265-43	Sequence 43, App1
C	26	81	5.1	1533	10	US-09-917-265-45	Sequence 45, App1
C	27	81	5.1	1599	10	US-09-917-265-38	Sequence 38, App1
C	28	81	5.1	1599	10	US-09-917-265-40	Sequence 40, App1
C	29	66	4.1	921	10	US-09-917-265-26	Sequence 26, App1
C	30	66	4.1	921	10	US-09-917-265-28	Sequence 28, App1
C	31	66	4.1	921	12	US-10-079-616-6	Sequence 6, App1
C	32	66	4.1	985	10	US-09-917-265-55	Sequence 55, App1
C	33	66	4.1	985	10	US-09-917-265-57	Sequence 57, App1
C	34	66	4.1	987	10	US-09-917-265-29	Sequence 29, App1
C	35	66	4.1	987	10	US-09-917-265-31	Sequence 31, App1
C	36	66	3.9	2193	12	US-10-079-616-5	Sequence 5, App1
C	37	63	3.9	921	12	US-10-079-616-7	Sequence 7, App1
C	38	55	3.7	60	10	US-09-917-265-83	Sequence 83, App1
C	39	55	3.7	60	10	US-09-917-265-84	Sequence 84, App1
C	40	59	3.7	660	10	US-09-734-014-6	Sequence 6, App1
C	41	59	3.7	660	10	US-09-836-866-4	Sequence 4, App1
C	42	59	3.7	689	12	US-10-079-616-26	Sequence 26, App1
C	43	59	3.7	762	9	US-09-826-025-21	Sequence 21, App1
C	44	59	3.7	1395	10	US-09-924-703-5	Sequence 5, App1
C	45	59	3.7	8578	10	US-09-828-825-1	Sequence 1, App1
C	46	59	3.7	8578	10	US-09-828-825-3	Sequence 3, App1
C	47	59	3.7	8608	10	US-09-828-825-7	Sequence 7, App1
C	48	59	3.7	8623	10	US-09-828-825-5	Sequence 5, App1
C	49	59	3.7	8629	10	US-09-828-825-15	Sequence 15, App1
C	50	59	3.7	8638	10	US-09-828-825-9	Sequence 9, App1
C	51	59	3.7	8644	10	US-09-828-825-13	Sequence 13, App1
C	52	59	3.7	8659	10	US-09-828-825-11	Sequence 11, App1
C	53	46	2.9	987	9	US-09-826-025-24	Sequence 24, App1
C	54	46	2.9	987	10	US-09-754-014-2	Sequence 2, App1
C	55	46	2.9	987	10	US-09-836-866-2	Sequence 3, App1
C	56	46	2.9	2262	10	US-09-924-703-3	Sequence 3, App1
C	57	35	2.2	51	10	US-09-917-265-96	Sequence 96, App1
C	58	27	1.7	37	10	US-09-917-265-99	Sequence 99, App1
C	59	27	1.7	79	12	US-10-079-616-24	Sequence 24, App1
C	60	24	1.5	987	10	US-09-754-014-3	Sequence 4, App1
C	61	24	1.5	987	10	US-09-754-014-4	Sequence 4, App1
C	62	22	1.4	22	10	US-09-917-265-94	Sequence 94, App1
C	63	22	1.4	22	10	US-09-917-265-97	Sequence 97, App1
C	64	22	1.4	38	10	US-09-917-265-95	Sequence 95, App1
C	65	21	1.3	44	12	US-10-079-616-14	Sequence 14, App1
C	66	21	1.3	21	10	US-09-917-265-98	Sequence 98, App1
C	67	19	1.2	19	10	US-09-791-500-16	Sequence 16, App1
C	68	19	1.2	2197	10	US-09-925-300-467	Sequence 467, App
C	69	15	1.2	3127	10	US-09-796-338A-1	Sequence 1, App1
C	70	15	1.2	6160	9	US-09-902-432-3	Sequence 3, App1
C	71	19	1.2	145831	10	US-09-964-708-79	Sequence 79, App1
C	72	19	1.2	145831	10	US-09-954-456-2115	Sequence 2115, App
C	73	18	1.1	28	10	US-09-917-265-85	Sequence 85, App1
C	74	18	1.1	37	10	US-09-917-265-87	Sequence 87, App1
C	75	18	1.1	246	10	US-09-923-876-3783	Sequence 3783, App
C	76	18	1.1	261	10	US-09-983-965-2681	Sequence 2681, App
C	77	18	1.1	481	10	US-09-833-381-382	Sequence 382, App
C	78	18	1.1	533	10	US-09-867-701-5960	Sequence 5960, App
C	79	18	1.1	582	10	US-09-998-598-1207	Sequence 1207, App
C	80	18	1.1	647	10	US-09-764-888-84	Sequence 84, App1
C	81	18	1.1	666	10	US-09-880-107-3775	Sequence 3775, App
C	82	18	1.1	718	10	US-09-925-300-7	Sequence 7, App1
C	83	18	1.1	731	10	US-09-925-301-6	Sequence 6, App1
C	84	18	1.1	735	9	US-09-954-531-1336	Sequence 1336, App
C	85	18	1.1	739	12	US-10-044-090-835	Sequence 818, App
C	86	18	1.1	847	10	US-09-925-301-315	Sequence 316, App
C	87	18	1.1	926	10	US-09-939-960-118	Sequence 118, App
C	88	18	1.1	1051	10	US-09-893-228-10	Sequence 10, App1
C	89	18	1.1	1051	9	US-09-804-409A-5	Sequence 5, App1
C	90	18	1.1	1401	10	US-09-730-989-1	Sequence 1, App1
C	91	18	1.1	1667	9	US-09-808-602-16	Sequence 16, App1
C	92	18	1.1				

C 239	15	1.0	378	10	US-09-815-343-781	Sequence 781, App	C 312	15	1.0	955	10	US-09-789-561-78	Sequence 78, App1
C 240	15	1.0	387	10	US-09-864-761-22729	Sequence 22729, A	C 313	15	1.0	996	9	US-09-938-842A-1711	Sequence 1711, Ap
C 241	15	1.0	400	10	US-09-864-761-10344	Sequence 10344, A	C 314	15	1.0	1066	9	US-09-764-868-390	Sequence 390, App
C 242	16	1.0	401	9	US-10-025-380-640	Sequence 640, App	C 315	15	1.0	1075	9	US-09-938-842A-3324	Sequence 3324, Ap
C 243	16	1.0	401	10	US-09-864-761-3936	Sequence 3936, Ap	C 316	15	1.0	1083	9	US-09-738-626-235	Sequence 235, App
C 244	15	1.0	401	10	US-09-735-705-277	Sequence 277, App	C 317	15	1.0	1096	10	US-09-771-161A-33	Sequence 33, App1
C 245	15	1.0	401	10	US-09-922-217-640	Sequence 640, App	C 318	15	1.0	1194	10	US-09-778-927A-22	Sequence 22, App1
C 246	15	1.0	401	10	US-09-833-263-640	Sequence 640, App	C 319	15	1.0	1248	10	US-09-815-242-6987	Sequence 6987, Ap
C 247	15	1.0	401	10	US-09-850-716A-277	Sequence 277, App	C 320	15	1.0	1362	10	US-09-822-830A-19	Sequence 19, App1
C 248	15	1.0	401	10	US-09-887-778-277	Sequence 277, App	C 321	15	1.0	1374	10	US-09-925-302-259	Sequence 259, App
C 249	15	1.0	406	10	US-09-950-352-3389	Sequence 3389, Ap	C 322	15	1.0	1422	10	US-09-880-107-2208	Sequence 2208, Ap
C 250	15	1.0	410	9	US-10-025-380-677	Sequence 677, App	C 323	15	1.0	1457	9	US-09-764-868-374	Sequence 374, App
C 251	15	1.0	410	10	US-09-922-217-677	Sequence 677, App	C 324	15	1.0	1467	9	US-09-938-842A-1826	Sequence 1826, Ap
C 252	15	1.0	410	10	US-09-833-263-677	Sequence 677, App	C 325	15	1.0	1470	10	US-09-073-009-130	Sequence 130, App
C 253	15	1.0	415	10	US-09-783-590-2517	Sequence 2517, Ap	C 326	15	1.0	1470	10	US-09-073-009-130	Sequence 130, App
C 254	15	1.0	436	9	US-09-796-692-2873	Sequence 2873, Ap	C 327	15	1.0	1588	10	US-09-960-253-144	Sequence 144, App
C 255	15	1.0	440	10	US-09-864-761-28236	Sequence 28236, A	C 328	15	1.0	1621	10	US-09-834-975-904	Sequence 904, App
C 256	15	1.0	446	9	US-10-045-935-1405	Sequence 1405, Ap	C 329	15	1.0	1621	10	US-09-834-975-904	Sequence 904, App
C 257	15	1.0	446	9	US-09-878-178-1405	Sequence 1405, Ap	C 330	15	1.0	1647	9	US-09-938-842A-1710	Sequence 1710, Ap
C 258	15	1.0	446	10	US-09-864-761-20659	Sequence 20659, A	C 331	15	1.0	1651	12	US-10-044-090-506	Sequence 506, App
C 259	15	1.0	449	5	US-10-015-219-481	Sequence 481, App	C 332	15	1.0	1683	10	US-09-943-075A-8	Sequence 8, App1
C 260	15	1.0	449	10	US-09-777-564-481	Sequence 481, App	C 333	15	1.0	1683	10	US-09-801-368-81	Sequence 81, App1
C 261	15	1.0	449	10	US-09-864-761-10970	Sequence 10970, A	C 334	15	1.0	1692	10	US-09-815-242-6121	Sequence 6121, Ap
C 262	15	1.0	452	10	US-09-864-761-1557	Sequence 1557, Ap	C 335	15	1.0	1755	9	US-09-938-842A-554	Sequence 554, App
C 263	15	1.0	452	10	US-09-864-761-18316	Sequence 18316, A	C 336	15	1.0	1796	10	US-09-771-838A-17	Sequence 17, App1
C 264	15	1.0	454	10	US-09-864-761-15619	Sequence 15619, A	C 337	15	1.0	1835	12	US-10-044-090-649	Sequence 649, App
C 265	15	1.0	454	10	US-09-925-300-390	Sequence 390, App	C 338	15	1.0	1840	10	US-09-954-456-723	Sequence 723, App
C 266	15	1.0	455	10	US-09-864-761-4352	Sequence 4352, App	C 339	15	1.0	1845	10	US-09-771-838A-5	Sequence 5, App1
C 267	15	1.0	464	10	US-09-864-761-14967	Sequence 14967, A	C 340	15	1.0	1849	9	US-10-136-511-1	Sequence 1, App1
C 268	15	1.0	465	10	US-09-864-761-3275	Sequence 3275, App	C 341	15	1.0	1849	9	US-09-345-790-1	Sequence 1, App1
C 269	15	1.0	465	10	US-09-880-107-2003	Sequence 2003, Ap	C 342	15	1.0	1871	10	US-09-862-007-3	Sequence 3, App1
C 270	15	1.0	466	10	US-09-864-761-2471	Sequence 2471, Ap	C 343	15	1.0	1905	9	US-09-938-842A-5139	Sequence 5139, Ap
C 271	15	1.0	465	10	US-09-864-761-5970	Sequence 5970, Ap	C 344	15	1.0	1914	10	US-09-954-456-504	Sequence 504, App
C 272	15	1.0	470	10	US-09-864-761-6046	Sequence 6046, Ap	C 345	15	1.0	1914	10	US-09-860-107-2172	Sequence 2172, Ap
C 273	15	1.0	471	10	US-09-728-445-684	Sequence 684, App	C 346	15	1.0	1954	10	US-09-834-975-980	Sequence 980, App
C 274	15	1.0	473	10	US-09-925-301-325	Sequence 325, App	C 347	15	1.0	1964	9	US-09-764-904-134	Sequence 134, App
C 275	15	1.0	475	10	US-09-864-761-1857	Sequence 1857, App	C 348	15	1.0	1964	10	US-09-764-904-134	Sequence 134, App
C 276	15	1.0	478	10	US-09-864-761-1520	Sequence 1520, Ap	C 349	15	1.0	1964	12	US-10-080-455-2	Sequence 2, App1
C 277	15	1.0	484	10	US-09-864-761-2222	Sequence 2222, Ap	C 350	15	1.0	1964	12	US-10-080-455-2	Sequence 2, App1
C 278	15	1.0	487	10	US-09-864-761-15253	Sequence 15253, A	C 351	15	1.0	1964	12	US-10-116-378-27	Sequence 27, App1
C 279	15	1.0	487	10	US-09-864-761-19201	Sequence 19201, A	C 352	15	1.0	1965	9	US-09-938-842A-4556	Sequence 4556, Ap
C 280	15	1.0	501	10	US-09-864-761-6915	Sequence 6915, Ap	C 353	15	1.0	1971	10	US-09-864-761-2815	Sequence 2815, Ap
C 281	15	1.0	509	10	US-09-563-817-159	Sequence 159, App	C 354	15	1.0	2000	9	US-09-938-842A-3580	Sequence 3580, Ap
C 282	15	1.0	511	10	US-09-880-107-451	Sequence 451, App	C 355	15	1.0	2000	9	US-09-938-842A-2286	Sequence 2286, Ap
C 283	15	1.0	513	10	US-09-864-761-13072	Sequence 13072, A	C 356	15	1.0	2019	9	US-09-801-368-195	Sequence 195, App
C 284	15	1.0	518	10	US-09-867-701-4793	Sequence 4793, A	C 357	15	1.0	2037	9	US-09-738-626-2495	Sequence 2495, App
C 285	15	1.0	522	10	US-09-864-761-12370	Sequence 12370, A	C 358	15	1.0	2046	10	US-09-771-838A-6	Sequence 6, App1
C 286	15	1.0	538	10	US-09-728-446-797	Sequence 797, App	C 359	15	1.0	2100	10	US-09-862-007-1	Sequence 1, App1
C 287	15	1.0	563	10	US-09-925-300-213	Sequence 213, App	C 360	15	1.0	2101	10	US-09-822-830A-50	Sequence 50, App1
C 288	15	1.0	566	10	US-09-815-343-464	Sequence 464, App	C 361	15	1.0	2218	10	US-09-954-456-57	Sequence 57, App1
C 289	15	1.0	568	10	US-09-864-761-15365	Sequence 15365, A	C 362	15	1.0	2218	10	US-09-954-456-596	Sequence 656, App
C 290	15	1.0	572	5	US-10-040-739-1354	Sequence 1354, Ap	C 363	15	1.0	2220	12	US-10-044-090-483	Sequence 483, App
C 291	15	1.0	576	10	US-09-864-761-9688	Sequence 9688, Ap	C 364	15	1.0	2271	10	US-09-919-585-1	Sequence 1, App1
C 292	15	1.0	576	10	US-09-920-300A-1018	Sequence 1018, Ap	C 365	15	1.0	2281	10	US-09-900-497-1	Sequence 1, App1
C 293	15	1.0	576	12	US-10-033-528-1018	Sequence 1018, Ap	C 366	15	1.0	2442	10	US-09-827-949-3	Sequence 3, App1
C 294	15	1.0	576	12	US-10-033-528-1835	Sequence 1835, Ap	C 367	15	1.0	2634	10	US-09-331-340-7	Sequence 7, App1
C 295	15	1.0	578	10	US-09-598-598-1023	Sequence 1023, App	C 368	15	1.0	2634	10	US-09-948-369-7	Sequence 7, App1
C 296	15	1.0	579	10	US-09-864-761-31501	Sequence 31501, A	C 369	15	1.0	2661	9	US-10-039-272-1	Sequence 27, App1
C 297	15	1.0	585	10	US-09-864-761-15395	Sequence 15395, A	C 370	15	1.0	2709	9	US-09-938-842A-297	Sequence 297, App
C 298	15	1.0	585	10	US-09-815-343-660	Sequence 660, App	C 371	15	1.0	2801	9	US-09-764-868-27	Sequence 27, App1
C 299	15	1.0	592	10	US-09-815-343-776	Sequence 776, App	C 372	15	1.0	2837	10	US-09-938-842A-11	Sequence 11, App1
C 300	15	1.0	640	9	US-10-025-380-630	Sequence 630, App	C 373	15	1.0	2839	10	US-09-909-775-1	Sequence 1, App1
C 301	15	1.0	640	10	US-09-922-217-630	Sequence 630, App	C 374	15	1.0	2889	10	US-09-891-216-9	Sequence 9, App1
C 302	15	1.0	640	10	US-09-833-263-630	Sequence 630, App	C 375	15	1.0	2889	10	US-09-891-216-18	Sequence 18, App1
C 303	15	1.0	708	10	US-09-770-149-220	Sequence 220, App	C 376	15	1.0	3023	10	US-09-079-892-4	Sequence 4, App1
C 304	15	1.0	714	10	US-09-864-761-19558	Sequence 19598, A	C 377	15	1.0	3048	12	US-10-044-090-685	Sequence 685, App
C 305	15	1.0	728	9	US-10-036-500-53	Sequence 53, App1	C 378	15	1.0	3228	10	US-09-801-368-183	Sequence 183, App
C 306	15	1.0	756	10	US-09-984-186-17	Sequence 17, App1	C 379	15	1.0	3313	10	US-09-764-846-83	Sequence 83, App1
C 307	15	1.0	758	10	US-09-510-943-438	Sequence 438, App	C 380	15	1.0	3505	9	US-09-954-456-1360	Sequence 1360, Ap
C 308	15	1.0	758	10	US-09-813-655-29	Sequence 29, App1	C 381	15	1.0	3505	9	US-09-954-456-1360	Sequence 1360, Ap
C 309	15	1.0	924	10	US-09-917-800A-1572	Sequence 1572, Ap	C 382	15	1.0	3914	12	US-10-044-090-148	Sequence 148, App
C 310	15	1.0	929	9	US-10-001-835-61	Sequence 61, App1	C 383	15	1.0	3965	10	US-09-801-368-113	Sequence 113, App
C 311	15	1.0	955	10	US-09-785-561-51	Sequence 51, App1	C 384	15	1.0	4316	10	US-09-880-107-3713	Sequence 3713, Ap

C 385	16	1.0	4415	9	US-10-045-180A-1	Sequence 1, Appl1	C 458	15	0.9	219	10	US-09-815-242-4407	Sequence 4407, Ap
C 386	16	1.0	4415	12	US-10-013-770-1	Sequence 1, Appl1	459	15	0.9	221	9	US-10-046-935-922	Sequence 922, App
C 387	16	1.0	4439	12	US-10-044-090-295	Sequence 295, App	460	15	0.9	221	9	US-09-878-178-922	Sequence 922, App
C 388	16	1.0	4656	10	US-09-891-216-6	Sequence 6, Appl1	461	15	0.9	225	9	US-09-796-692-1196	Sequence 1196, Ap
C 389	16	1.0	4963	10	US-09-764-870-606	Sequence 606, App	462	15	0.9	228	10	US-09-864-761-19809	Sequence 19809, A
C 390	16	1.0	4963	10	US-09-764-860-694	Sequence 694, App	463	15	0.9	230	10	US-09-823-876-4983	Sequence 4983, Ap
C 391	16	1.0	5273	10	US-09-070-927A-362	Sequence 362, App	464	15	0.9	231	10	US-09-815-242-6876	Sequence 6876, Ap
C 392	16	1.0	5262	10	US-09-030-482B-18	Sequence 18, Appl	465	15	0.9	232	10	US-09-764-864-1669	Sequence 1669, Ap
C 393	16	1.0	5627	9	US-10-098-841-227	Sequence 227, App	466	15	0.9	233	10	US-09-923-876-4978	Sequence 4978, Ap
C 394	16	1.0	6226	10	US-09-827-949-1	Sequence 1, Appl1	467	15	0.9	234	10	US-09-815-242-8026	Sequence 8026, Ap
C 395	16	1.0	6415	10	US-09-070-927A-275	Sequence 275, App	468	15	0.9	234	10	US-09-815-242-8704	Sequence 8704, Ap
C 396	16	1.0	6698	10	US-09-764-869-2416	Sequence 2416, Ap	469	15	0.9	234	10	US-09-815-242-9003	Sequence 9003, Ap
C 397	16	1.0	6816	10	US-09-935-541-1	Sequence 1, Appl1	470	15	0.9	239	10	US-09-878-574-1595	Sequence 1595, Ap
C 398	16	1.0	6855	10	US-09-935-541-3	Sequence 3, Appl1	471	15	0.9	240	10	US-09-983-965-4422	Sequence 4422, Ap
C 400	16	1.0	7639	12	US-10-033-026-9	Sequence 9, Appl1	472	15	0.9	241	10	US-09-864-761-17220	Sequence 17220, A
C 401	16	1.0	7787	10	US-09-971-536-28	Sequence 28, Appl	473	15	0.9	243	10	US-09-833-381-2010	Sequence 2010, Ap
C 402	16	1.0	9224	9	US-09-954-456-25006	Sequence 2006, Ap	474	15	0.9	243	10	US-09-960-352-9469	Sequence 9469, Ap
C 403	16	1.0	9669	10	US-10-108-605-254	Sequence 254, App	475	15	0.9	246	10	US-09-754-997A-21	Sequence 21, Appl
C 404	16	1.0	10194	10	US-09-764-869-2072	Sequence 2072, Ap	476	15	0.9	247	10	US-09-878-574-15699	Sequence 15699, A
C 405	16	1.0	10629	10	US-09-070-927A-91	Sequence 91, Appl	477	15	0.9	247	10	US-09-833-381-498	Sequence 498, App
C 406	16	1.0	10636	10	US-09-954-314-15	Sequence 15, Appl	478	15	0.9	249	10	US-09-974-300-7978	Sequence 7978, Ap
C 407	16	1.0	13968	10	US-09-070-927A-74	Sequence 74, Appl	479	15	0.9	250	10	US-09-880-107-2079	Sequence 2079, Ap
C 408	16	1.0	15613	10	US-09-764-869-2224	Sequence 2224, Ap	480	15	0.9	254	10	US-09-783-590-11596	Sequence 11596, A
C 409	16	1.0	23607	10	US-09-764-877-3626	Sequence 3626, Ap	482	15	0.9	255	10	US-09-878-574-10445	Sequence 10445, A
C 410	16	1.0	32038	10	US-09-764-878-292	Sequence 292, App	483	15	0.9	259	10	US-09-878-574-10647	Sequence 10647, A
C 411	16	1.0	32191	10	US-09-764-864-1678	Sequence 1678, Ap	484	15	0.9	262	10	US-09-923-876-607	Sequence 607, App
C 412	16	1.0	32768	10	US-09-070-927A-17	Sequence 17, Appl	485	15	0.9	263	10	US-09-878-574-13024	Sequence 13024, A
C 413	16	1.0	90050	10	US-09-893-238-5	Sequence 5, Appl1	486	15	0.9	264	10	US-09-864-761-31242	Sequence 31242, A
C 414	16	1.0	147309	10	US-09-742-312-3	Sequence 3, Appl1	487	15	0.9	266	10	US-09-983-965-855	Sequence 855, App
C 415	16	1.0	174393	10	US-09-804-471A-3	Sequence 3, Appl1	488	15	0.9	268	10	US-09-923-876-734	Sequence 734, App
C 416	16	1.0	180216	10	US-09-835-232-6	Sequence 6, Appl1	489	15	0.9	268	10	US-09-923-876-4579	Sequence 4579, Ap
C 417	16	1.0	180216	10	US-09-835-232-6	Sequence 6, Appl1	490	15	0.9	268	10	US-09-923-876-4579	Sequence 4579, Ap
C 418	16	1.0	197997	10	US-09-822-246-3	Sequence 3, Appl1	491	15	0.9	270	9	US-09-878-574-8975	Sequence 8975, Ap
C 419	16	1.0	368004	10	US-09-949-654-3	Sequence 3, Appl1	492	15	0.9	270	9	US-10-046-935-199	Sequence 199, App
C 420	16	1.0	684973	10	US-09-263-959-1	Sequence 1, Appl1	493	15	0.9	272	10	US-09-878-574-5538	Sequence 5538, Ap
C 421	16	1.0	330940	9	US-09-738-626-1	Sequence 1, Appl1	494	15	0.9	272	10	US-09-878-574-7856	Sequence 7856, Ap
C 422	15	0.9	38	9	US-10-079-818-25	Sequence 25, Appl	495	15	0.9	276	10	US-09-969-373-430	Sequence 373, Appl
C 423	15	0.9	48	9	US-10-079-802-19	Sequence 19, Appl	496	15	0.9	279	10	US-09-972-714-3	Sequence 714, Appl
C 424	15	0.9	48	9	US-09-359-595-25	Sequence 25, Appl	497	15	0.9	280	10	US-09-878-574-11701	Sequence 11701, A
C 425	15	0.9	51	10	US-09-320-337-37	Sequence 37, Appl	498	15	0.9	282	9	US-09-796-692-1131	Sequence 6131, Ap
C 426	15	0.9	51	10	US-09-320-337-39	Sequence 39, Appl	499	15	0.9	282	10	US-09-923-876-4540	Sequence 4540, Ap
C 427	15	0.9	65	9	US-09-900-379-118	Sequence 18, App	500	15	0.9	283	10	US-09-294-093B-1863	Sequence 1863, Ap
C 428	15	0.9	65	10	US-09-848-164-118	Sequence 118, App	501	15	0.9	284	9	US-09-796-692-2731	Sequence 2731, Ap
C 429	15	0.9	82	10	US-09-978-152-17	Sequence 118, App	502	15	0.9	285	10	US-09-294-093B-5776	Sequence 5776, Ap
C 430	15	0.9	85	9	US-09-991-470-5	Sequence 5, Appl1	503	15	0.9	290	10	US-09-783-590-9187	Sequence 9187, Ap
C 431	15	0.9	88	9	US-09-908-153B-25	Sequence 25, Appl	504	15	0.9	291	10	US-09-920-300A-192	Sequence 192, App
C 432	15	0.9	90	9	US-09-908-153B-20	Sequence 20, Appl	505	15	0.9	291	12	US-10-033-528-192	Sequence 192, App
C 433	15	0.9	106	10	US-09-864-761-29594	Sequence 29594, A	506	15	0.9	295	10	US-09-960-352-13939	Sequence 13939, A
C 434	15	0.9	106	10	US-09-294-093B-1825	Sequence 1825, Ap	507	15	0.9	299	10	US-09-764-877-585	Sequence 585, App
C 435	15	0.9	114	10	US-09-783-590-3862	Sequence 3862, Ap	508	15	0.9	300	10	US-09-864-761-21688	Sequence 21688, A
C 436	15	0.9	118	10	US-09-867-701-9797	Sequence 9797, Ap	509	15	0.9	304	10	US-09-867-701-7371	Sequence 7371, Ap
C 437	15	0.9	127	10	US-09-864-761-30134	Sequence 30134, A	510	15	0.9	306	8	US-08-424-5508-27	Sequence 27, Appl
C 438	15	0.9	128	10	US-09-969-373-68	Sequence 68, Appl	511	15	0.9	306	8	US-08-424-5508-161	Sequence 161, App
C 439	15	0.9	135	10	US-09-962-436-547	Sequence 547, App	512	15	0.9	309	10	US-09-864-761-19783	Sequence 19783, A
C 440	15	0.9	136	10	US-09-864-761-19095	Sequence 19095, A	513	15	0.9	313	10	US-09-864-761-23071	Sequence 23071, A
C 441	15	0.9	136	10	US-09-864-761-30915	Sequence 30915, A	514	15	0.9	313	10	US-09-864-761-28315	Sequence 28315, A
C 442	15	0.9	137	10	US-09-864-761-27259	Sequence 27259, A	515	15	0.9	313	10	US-09-783-590-5646	Sequence 5646, Ap
C 443	15	0.9	149	10	US-09-864-761-23828	Sequence 23828, A	516	15	0.9	313	10	US-09-764-877-3162	Sequence 3162, Ap
C 444	15	0.9	154	10	US-09-864-761-31395	Sequence 31395, A	517	15	0.9	313	10	US-09-764-877-3163	Sequence 3163, Ap
C 445	15	0.9	155	10	US-09-878-574-11515	Sequence 11515, A	518	15	0.9	318	9	US-09-728-444-919	Sequence 919, App
C 446	15	0.9	172	9	US-09-796-692-6409	Sequence 6409, Ap	519	15	0.9	318	10	US-09-983-965-980	Sequence 980, App
C 447	15	0.9	172	9	US-09-796-692-6671	Sequence 6671, Ap	520	15	0.9	322	10	US-09-783-590-583	Sequence 583, App
C 448	15	0.9	176	10	US-09-815-242-893	Sequence 893, App	521	15	0.9	322	10	US-09-746-491-65	Sequence 65, Appl
C 449	15	0.9	178	10	US-09-864-761-16974	Sequence 16974, A	522	15	0.9	323	10	US-09-090-672B-15	Sequence 15, Appl
C 450	15	0.9	180	10	US-09-864-761-23564	Sequence 23564, A	523	15	0.9	331	10	US-09-800-729-210	Sequence 210, App
C 451	15	0.9	184	10	US-09-833-381-503	Sequence 503, App	524	15	0.9	339	9	US-09-796-692-5754	Sequence 5754, Ap
C 452	15	0.9	187	10	US-09-864-761-17616	Sequence 17616, A	525	15	0.9	341	10	US-09-983-965-4712	Sequence 4712, Ap
C 453	15	0.9	191	10	US-09-770-696-220	Sequence 220, App	526	15	0.9	347	10	US-09-960-352-748	Sequence 748, Appl
C 454	15	0.9	198	10	US-09-783-590-672	Sequence 672, App	527	15	0.9	347	10	US-09-960-352-7842	Sequence 7842, Ap
C 455	15	0.9	201	10	US-09-923-876-2840	Sequence 2840, Ap	528	15	0.9	349	10	US-09-864-761-18855	Sequence 18855, A
C 456	15	0.9	206	9	US-09-754-853A-146	Sequence 146, App	529	15	0.9	350	10	US-09-560-863-501	Sequence 501, App
C 457	15	0.9	215	10	US-09-815-242-3646	Sequence 3646, Ap	530	15	0.9	350	10	US-09-867-701-5200	Sequence 5200, Ap

531	15	0.9	360	10	US-09-878-574-2383	Sequence 2383, Ap	604	15	0.9	475	10	US-09-864-761-382	Sequence 382, App
532	15	0.5	363	10	US-09-960-352-13964	Sequence 13964, A	605	15	0.9	477	10	US-09-864-761-146	Sequence 146, App
533	15	0.9	364	10	US-09-960-352-29	Sequence 29, App1	606	15	0.9	477	10	US-09-864-761-2112	Sequence 2112, App
534	15	0.9	367	9	US-09-796-682-4240	Sequence 4240, Ap	607	15	0.9	477	10	US-09-834-975-679	Sequence 679, App
535	15	0.9	367	10	US-09-878-574-1861	Sequence 1861, Ap	608	15	0.9	479	10	US-09-867-701-2739	Sequence 2739, Ap
536	15	0.9	369	10	US-09-878-574-2953	Sequence 2953, Ap	609	15	0.9	480	10	US-09-833-381-1502	Sequence 1502, Ap
537	15	0.9	372	10	US-09-867-701-10029	Sequence 10029, A	610	15	0.9	481	10	US-09-884-441-46	Sequence 46, App1
538	15	0.9	378	10	US-09-983-965-5478	Sequence 5478, Ap	611	15	0.9	482	10	US-09-864-761-1862	Sequence 1862, Ap
539	15	0.5	375	9	US-09-796-682-2837	Sequence 2837, Ap	612	15	0.9	483	10	US-09-563-817-234	Sequence 234, App
540	15	0.9	375	9	US-09-796-682-4850	Sequence 4850, Ap	613	15	0.9	484	10	US-09-070-9278-899	Sequence 899, App
541	15	0.9	380	10	US-09-963-965-5104	Sequence 5104, Ap	614	15	0.9	488	10	US-09-783-590-7218	Sequence 7218, App
542	15	0.9	381	10	US-09-878-574-1464	Sequence 1464, Ap	615	15	0.9	488	10	US-09-783-590-8835	Sequence 8835, Ap
543	15	0.9	382	10	US-09-867-701-5454	Sequence 5454, Ap	616	15	0.9	488	10	US-09-974-300-1777	Sequence 1777, Ap
544	15	0.9	383	10	US-09-833-381-685	Sequence 685, App	617	15	0.9	490	10	US-09-834-975-440	Sequence 440, App
545	15	0.9	384	9	US-09-938-88428-2110	Sequence 2110, Ap	618	15	0.9	494	10	US-09-777-9218-126	Sequence 126, App
546	15	0.9	385	10	US-09-960-352-8029	Sequence 8029, Ap	619	15	0.9	495	10	US-09-864-761-6354	Sequence 6354, App
547	15	0.9	387	10	US-09-770-791-69	Sequence 69, App1	620	15	0.9	496	10	US-09-864-761-11742	Sequence 11742, A
548	15	0.9	391	10	US-09-878-574-4045	Sequence 4045, Ap	621	15	0.9	495	10	US-09-783-590-519	Sequence 519, App
549	15	0.9	396	10	US-09-867-701-5741	Sequence 5741, Ap	622	15	0.9	497	10	US-09-878-574-4516	Sequence 4516, Ap
550	15	0.9	400	10	US-09-960-352-3498	Sequence 3498, Ap	623	15	0.9	497	10	US-09-998-598-1407	Sequence 1407, Ap
551	15	0.9	403	10	US-09-867-550-321	Sequence 321, App	624	15	0.9	499	9	US-10-046-935-2109	Sequence 2109, Ap
552	15	0.9	403	10	US-09-880-107-2080	Sequence 2080, Ap	625	15	0.9	502	10	US-09-878-178-2109	Sequence 2109, Ap
553	15	0.9	404	10	US-09-833-381-2030	Sequence 2030, Ap	626	15	0.9	502	10	US-09-864-761-16356	Sequence 16356, A
554	15	0.9	404	10	US-09-960-352-7349	Sequence 7349, Ap	627	15	0.9	506	9	US-09-764-904-39	Sequence 39, App1
555	15	0.9	405	10	US-09-864-761-3651	Sequence 3651, Ap	628	15	0.9	506	10	US-09-764-860-298	Sequence 298, App
556	15	0.9	407	10	US-09-867-550-747	Sequence 747, App	629	15	0.9	508	10	US-09-998-598-775	Sequence 775, App
557	15	0.9	408	10	US-09-783-590-1129	Sequence 1129, Ap	630	15	0.9	509	10	US-09-867-701-4137	Sequence 4137, App
558	15	0.9	412	10	US-09-983-965-445	Sequence 445, App	631	15	0.9	510	10	US-09-967-7688-310	Sequence 310, App
559	15	0.9	413	10	US-09-864-761-4588	Sequence 4588, Ap	632	15	0.9	512	10	US-09-956-004-35	Sequence 35, App1
560	15	0.9	413	10	US-09-924-0358-238	Sequence 238, App	633	15	0.9	516	10	US-09-834-975-377	Sequence 377, App
561	15	0.9	414	9	US-10-079-623-29	Sequence 29, App1	634	15	0.9	517	9	US-10-016-1578-56	Sequence 56, App1
562	15	0.9	415	10	US-09-867-550-753	Sequence 753, App	635	15	0.9	518	9	US-09-938-88428-2872	Sequence 2872, Ap
563	15	0.9	416	10	US-09-864-761-11382	Sequence 11382, A	636	15	0.9	519	9	US-09-796-682-4968	Sequence 468, App
564	15	0.9	425	10	US-09-728-445-452	Sequence 492, App	637	15	0.9	522	10	US-09-920-3008-669	Sequence 669, App
565	15	0.9	427	10	US-09-864-761-3027	Sequence 3027, Ap	638	15	0.9	522	10	US-09-998-598-252	Sequence 252, App
566	15	0.9	427	10	US-09-960-352-2847	Sequence 2847, Ap	639	15	0.9	522	12	US-10-033-528-669	Sequence 669, App
567	15	0.9	427	10	US-09-960-352-6215	Sequence 6215, Ap	640	15	0.9	525	9	US-09-854-133-644	Sequence 644, App
568	15	0.9	430	10	US-09-864-761-3602	Sequence 3602, Ap	641	15	0.9	525	10	US-09-833-979-314	Sequence 314, App
569	15	0.9	430	10	US-09-960-352-6022	Sequence 6022, Ap	642	15	0.9	525	10	US-09-995-494-6	Sequence 6, App1
570	15	0.9	434	10	US-09-735-705-26	Sequence 26, App1	643	15	0.9	526	10	US-09-864-761-6903	Sequence 6903, Ap
571	15	0.9	434	10	US-09-850-7168-26	Sequence 26, App1	644	15	0.9	531	10	US-09-884-441-6	Sequence 6, App1
572	15	0.9	434	10	US-09-897-778-26	Sequence 26, App1	645	15	0.9	532	10	US-09-604-2878-432	Sequence 432, App1
573	15	0.9	435	10	US-09-960-352-7143	Sequence 7143, Ap	646	15	0.9	532	10	US-09-998-598-374	Sequence 374, App
574	15	0.9	437	10	US-09-735-705-74	Sequence 74, App1	647	15	0.9	532	10	US-09-998-598-1117	Sequence 1117, Ap
575	15	0.9	437	10	US-09-850-7168-74	Sequence 74, App1	648	15	0.9	532	12	US-10-007-805-432	Sequence 432, App
576	15	0.9	437	10	US-09-897-778-74	Sequence 74, App1	649	15	0.9	533	10	US-09-951-107-8	Sequence 8, App1
577	15	0.9	438	9	US-10-051-643-51	Sequence 51, App1	650	15	0.9	537	10	US-09-864-761-12317	Sequence 12317, A
578	15	0.9	438	9	US-09-880-505-51	Sequence 51, App1	651	15	0.9	541	10	US-09-864-761-7474	Sequence 7474, Ap
579	15	0.9	438	10	US-09-960-352-821	Sequence 821, App	652	15	0.9	541	10	US-09-864-761-7879	Sequence 7879, Ap
580	15	0.9	440	10	US-09-983-965-3055	Sequence 3055, Ap	653	15	0.9	547	10	US-09-974-300-2567	Sequence 2567, Ap
581	15	0.9	446	10	US-09-983-965-2002	Sequence 2002, Ap	654	15	0.9	558	9	US-10-040-739-1453	Sequence 1453, Ap
582	15	0.9	447	9	US-09-796-682-3583	Sequence 3583, Ap	655	15	0.9	561	10	US-09-864-761-14868	Sequence 14868, A
583	15	0.9	448	10	US-09-864-761-6583	Sequence 6582, App	656	15	0.9	561	10	US-09-815-837-8	Sequence 8, App1
584	15	0.9	448	10	US-09-920-3008-982	Sequence 982, App	657	15	0.9	562	9	US-09-796-682-8197	Sequence 8197, App
585	15	0.9	448	12	US-10-033-528-982	Sequence 982, App	658	15	0.9	563	9	US-09-796-682-9733	Sequence 8733, Ap
586	15	0.9	449	10	US-09-864-761-3001	Sequence 3001, App	659	15	0.9	563	10	US-09-764-887-917	Sequence 917, App
587	15	0.9	449	10	US-09-864-761-3785	Sequence 3785, Ap	660	15	0.9	566	10	US-09-864-761-13721	Sequence 13721, A
588	15	0.9	451	10	US-09-864-761-15284	Sequence 15284, A	661	15	0.9	566	10	US-09-864-761-18697	Sequence 18697, A
589	15	0.9	460	10	US-09-864-761-465	Sequence 465, App	662	15	0.9	570	10	US-09-864-761-61831	Sequence 6831, Ap
590	15	0.9	460	10	US-09-864-761-14540	Sequence 14540, A	663	15	0.9	570	10	US-09-864-761-1227	Sequence 227, App
591	15	0.9	461	10	US-09-811-284-60	Sequence 60, App1	664	15	0.9	570	10	US-09-880-107-3177	Sequence 3177, App
592	15	0.9	462	9	US-09-796-682-3430	Sequence 3430, App	665	15	0.9	573	10	US-09-864-761-8258	Sequence 8258, Ap
593	15	0.9	462	10	US-09-978-350-1332	Sequence 1332, App	666	15	0.9	577	10	US-09-841-132-418	Sequence 418, App
594	15	0.9	463	10	US-09-793-590-1273	Sequence 1233, App	667	15	0.9	577	10	US-09-864-761-8117	Sequence 8117, App
595	15	0.9	463	10	US-09-864-761-4840	Sequence 4840, App	668	15	0.9	579	10	US-09-864-761-19885	Sequence 19885, A
596	15	0.9	470	10	US-09-770-444-207	Sequence 207, App	669	15	0.9	582	10	US-09-815-837-12	Sequence 12, App1
597	15	0.9	471	10	US-09-864-761-4016	Sequence 4016, Ap	670	15	0.9	585	10	US-09-864-761-13032	Sequence 13032, A
598	15	0.9	471	10	US-09-864-761-14353	Sequence 14353, A	671	15	0.9	587	10	US-09-864-761-13595	Sequence 13595, A
599	15	0.9	472	10	US-09-864-761-17282	Sequence 17282, A	672	15	0.9	592	10	US-09-864-761-7155	Sequence 7155, App
600	15	0.9	473	10	US-09-864-761-10566	Sequence 10506, A	673	15	0.9	593	10	US-09-864-761-16190	Sequence 16190, App
601	15	0.9	473	10	US-09-864-761-14713	Sequence 14713, A	674	15	0.9	599	10	US-09-864-761-7472	Sequence 7472, Ap
602	15	0.9	474	10	US-09-864-761-2361	Sequence 2361, App	675	15	0.9	599	10	US-09-872-153-14	Sequence 14, App1
603	15	0.9	474	10	US-09-864-761-2554	Sequence 2594, App	676	15	0.9	600	10	US-09-864-761-7097	Sequence 7097, App

C 677	15	0.9	600	10	US-09-974-300-333	Sequence 333, App	C 750	15	0.9	1151	10	US-09-764-864-214	Sequence 214, App
C 678	15	0.9	601	10	US-09-777-921A-125	Sequence 125, App	C 751	15	0.9	1164	9	US-10-051-683-193	Sequence 193, App
C 679	15	0.9	620	9	US-10-040-739-1116	Sequence 1116, Ap	C 752	15	0.9	1164	9	US-09-880-505-193	Sequence 193, App
C 680	15	0.9	630	10	US-09-815-837-54	Sequence 54, Appl	C 753	15	0.9	1173	10	US-09-815-242-6586	Sequence 6586, Ap
C 681	15	0.9	636	10	US-09-925-297-278	Sequence 278, App	C 754	15	0.9	1176	9	US-09-982-598-413	Sequence 413, App
C 682	15	0.9	642	10	US-09-815-837-32	Sequence 32, Appl	C 755	15	0.9	1176	9	US-09-989-938A-413	Sequence 413, App
C 683	15	0.9	642	10	US-09-815-837-52	Sequence 52, Appl	C 756	15	0.9	1176	9	US-10-063-547-87	Sequence 87, Appl
C 684	15	0.9	642	10	US-09-815-837-55	Sequence 55, Appl	C 757	15	0.9	1176	9	US-09-989-735-413	Sequence 413, App
C 685	15	0.9	642	10	US-09-815-837-77	Sequence 77, Appl	C 758	15	0.9	1176	9	US-09-989-444-413	Sequence 413, App
C 686	15	0.9	642	10	US-09-879-536-82	Sequence 82, Appl	C 759	15	0.9	1176	9	US-09-989-730-413	Sequence 413, App
C 687	15	0.9	644	10	US-09-864-761-31562	Sequence 31562, A	C 760	15	0.9	1176	9	US-09-990-436-413	Sequence 413, App
C 688	15	0.9	647	10	US-09-815-837-78	Sequence 78, Appl	C 761	15	0.9	1176	9	US-09-991-181-413	Sequence 413, App
C 689	15	0.9	649	10	US-09-822-849A-573	Sequence 573, Appl	C 762	15	0.9	1176	9	US-09-993-687-413	Sequence 413, App
C 690	15	0.9	649	10	US-09-747-155-142	Sequence 142, Appl	C 763	15	0.9	1176	9	US-09-989-734-413	Sequence 413, App
C 691	15	0.9	663	10	US-09-815-837-36	Sequence 36, Appl	C 764	15	0.9	1176	9	US-09-997-653-413	Sequence 413, App
C 692	15	0.9	664	10	US-09-919-580-15	Sequence 15, Appl	C 765	15	0.9	1176	9	US-10-174-590-293	Sequence 293, App
C 693	15	0.9	678	10	US-09-879-792-30	Sequence 30, Appl	C 766	15	0.9	1176	9	US-10-176-758-293	Sequence 293, App
C 694	15	0.9	687	10	US-09-910-943-284	Sequence 284, App	C 767	15	0.9	1176	10	US-09-989-722-413	Sequence 413, App
C 695	15	0.9	688	10	US-09-879-792-32	Sequence 32, Appl	C 768	15	0.9	1176	10	US-09-989-723-413	Sequence 413, App
C 696	15	0.9	690	10	US-09-864-761-19663	Sequence 19663, A	C 769	15	0.9	1176	10	US-09-989-729-413	Sequence 413, App
C 697	15	0.9	691	9	US-10-040-739-425	Sequence 425, App	C 770	15	0.9	1176	10	US-09-989-727-413	Sequence 413, App
C 698	15	0.9	694	10	US-09-770-149-288	Sequence 288, App	C 771	15	0.9	1176	10	US-09-989-731-413	Sequence 413, App
C 699	15	0.9	699	9	US-10-044-716-3	GENERAL INFORMATI	C 772	15	0.9	1176	10	US-09-989-732-413	Sequence 413, App
C 700	15	0.9	699	10	US-09-897-322-1	Sequence 1, Appl1	C 773	15	0.9	1176	10	US-09-991-072-413	Sequence 413, App
C 701	15	0.9	699	10	US-09-974-300-2766	Sequence 2766, Ap	C 774	15	0.9	1176	10	US-09-990-442-413	Sequence 413, App
C 702	15	0.9	708	9	US-09-479-040-24	Sequence 24, Appl	C 775	15	0.9	1176	10	US-09-990-163-413	Sequence 413, App
C 703	15	0.9	725	10	US-09-770-149-131	Sequence 131, App	C 776	15	0.9	1176	10	US-09-993-604-413	Sequence 413, App
C 704	15	0.9	735	9	US-09-991-470-26	Sequence 26, Appl	C 777	15	0.9	1176	10	US-09-990-456-413	Sequence 413, App
C 705	15	0.9	750	10	US-09-887-576-801	Sequence 801, App	C 778	15	0.9	1176	10	US-09-989-721-413	Sequence 413, App
C 706	15	0.9	752	10	US-09-974-300-1503	Sequence 1503, Ap	C 779	15	0.9	1176	12	US-10-006-867-87	Sequence 87, Appl
C 707	15	0.9	762	10	US-09-815-242-7625	Sequence 7625, Ap	C 780	15	0.9	1176	12	US-10-052-586-293	Sequence 293, App
C 708	15	0.9	767	10	US-09-995-494-7	Sequence 7, Appl1	C 781	15	0.9	1179	12	US-10-007-693-85	Sequence 85, Appl
C 709	15	0.9	770	10	US-09-928-445-628	Sequence 628, App	C 782	15	0.9	1183	10	US-09-764-864-605	Sequence 605, App
C 710	15	0.9	774	10	US-09-764-864-567	Sequence 567, App	C 783	15	0.9	1191	10	US-09-864-761-81	Sequence 27183, A
C 711	15	0.9	809	9	US-10-202-193-233	Sequence 233, App	C 784	15	0.9	1192	9	US-09-861-682-2	Sequence 2, Appl1
C 712	15	0.9	816	9	US-09-766-543-9	Sequence 9, Appl1	C 785	15	0.9	1200	9	US-10-078-770-9	Sequence 9, Appl1
C 713	15	0.9	825	10	US-09-956-004-102	Sequence 102, App	C 786	15	0.9	1200	10	US-09-799-777-125	Sequence 125, App
C 714	15	0.9	825	9	US-10-081-643-74	Sequence 74, Appl	C 787	15	0.9	1224	9	US-09-938-642A-1113	Sequence 1113, Ap
C 715	15	0.9	825	9	US-09-860-505-73	Sequence 74, Appl	C 788	15	0.9	1230	10	US-09-070-922A-335	Sequence 335, App
C 716	15	0.9	840	10	US-09-766-543-11	Sequence 11, Appl	C 789	15	0.9	1232	9	US-09-938-842A-1538	Sequence 1538, Ap
C 717	15	0.9	840	10	US-09-822-849A-574	Sequence 574, Appl	C 790	15	0.9	1246	10	US-09-974-300-6296	Sequence 6296, Ap
C 718	15	0.9	890	9	US-09-938-842A-5118	Sequence 5118, Ap	C 791	15	0.9	1251	10	US-09-974-300-264	Sequence 264, App
C 719	15	0.9	900	10	US-09-853-625B-1	Sequence 1, Appl1	C 792	15	0.9	1254	10	US-09-815-242-96157	Sequence 6157, Ap
C 720	15	0.9	908	9	US-09-976-673-3	Sequence 3, Appl1	C 793	15	0.9	1260	10	US-09-815-242-9694	Sequence 9694, Ap
C 721	15	0.9	913	10	US-09-974-300-4259	Sequence 4259, Ap	C 794	15	0.9	1261	10	US-09-898-533-10	Sequence 10, Appl1
C 722	15	0.9	922	10	US-09-770-445-411	Sequence 411, App	C 795	15	0.9	1265	10	US-09-371-307-1	Sequence 1, Appl1
C 723	15	0.9	927	10	US-09-886-055-278	Sequence 278, App	C 796	15	0.9	1298	10	US-09-925-301-85	Sequence 85, Appl
C 724	15	0.9	936	10	US-09-884-441-161	Sequence 161, App	C 797	15	0.9	1308	9	US-10-160-865-1	Sequence 1, Appl1
C 725	15	0.9	937	10	US-09-925-302-61	Sequence 61, Appl	C 798	15	0.9	1309	10	US-09-867-701-10864	Sequence 10864, A
C 726	15	0.9	951	10	US-09-841-132-118	Sequence 118, App	C 799	15	0.9	1320	10	US-09-727-238-1	Sequence 1, Appl1
C 727	15	0.9	960	10	US-09-974-300-506	Sequence 506, App	C 800	15	0.9	1325	9	US-09-989-920-85	Sequence 85, Appl1
C 728	15	0.9	963	9	US-09-738-626-1565	Sequence 1565, Ap	C 801	15	0.9	1330	10	US-09-974-300-1081	Sequence 1081, A
C 729	15	0.9	965	10	US-09-770-445-300	Sequence 300, App	C 802	15	0.9	1332	10	US-09-867-701-10891	Sequence 10891, A
C 730	15	0.9	967	9	US-09-895-913A-41	Sequence 41, Appl	C 803	15	0.9	1334	10	US-09-349-015-1	Sequence 1, Appl1
C 731	15	0.9	981	10	US-09-864-761-1948	Sequence 1948, Ap	C 804	15	0.9	1338	10	US-09-815-242-8842	Sequence 8842, Ap
C 732	15	0.9	981	10	US-09-862-027-9	Sequence 9, Appl1	C 805	15	0.9	1346	10	US-09-764-864-169	Sequence 169, App
C 733	15	0.9	990	9	US-09-938-842A-1960	Sequence 1960, App	C 806	15	0.9	1348	10	US-09-822-830A-404	Sequence 404, App
C 734	15	0.9	994	10	US-09-784-423-42	Sequence 42, Appl	C 807	15	0.9	1362	9	US-09-931-457A-30	Sequence 30, Appl1
C 735	15	0.9	999	10	US-09-816-894-12	Sequence 12, Appl	C 808	15	0.9	1371	10	US-09-815-242-6844	Sequence 6844, Ap
C 736	15	0.9	1017	9	US-09-938-842A-60	Sequence 60, Appl	C 809	15	0.9	1371	10	US-09-925-297-147	Sequence 147, App
C 737	15	0.9	1017	9	US-09-738-626-2676	Sequence 2676, Ap	C 810	15	0.9	1373	10	US-09-729-835-33	Sequence 33, Appl
C 738	15	0.9	1029	10	US-09-815-242-6966	Sequence 6966, Ap	C 811	15	0.9	1377	10	US-09-801-366-167	Sequence 167, App
C 739	15	0.9	1034	9	US-10-174-590-321	Sequence 321, App	C 812	15	0.9	1378	10	US-09-820-893-28	Sequence 28, Appl
C 740	15	0.9	1034	9	US-10-176-758-321	Sequence 321, App	C 813	15	0.9	1380	9	US-09-738-626-723	Sequence 723, App
C 741	15	0.9	1034	12	US-10-052-586-321	Sequence 321, App	C 814	15	0.9	1382	9	US-09-900-379-123	Sequence 123, App
C 742	15	0.9	1062	10	US-09-815-242-7467	Sequence 7467, Ap	C 815	15	0.9	1382	10	US-09-848-164-1133	Sequence 123, App
C 743	15	0.9	1065	9	US-09-938-842A-1466	Sequence 1466, Ap	C 816	15	0.9	1385	9	US-09-900-379-121	Sequence 121, App
C 744	15	0.9	1080	10	US-09-785-671-6	Sequence 6, Appl1	C 817	15	0.9	1385	10	US-09-848-164-121	Sequence 121, App
C 745	15	0.9	1086	9	US-09-938-842A-2128	Sequence 2128, App	C 818	15	0.9	1385	10	US-09-800-729-40	Sequence 40, Appl
C 746	15	0.9	1092	10	US-09-785-671-1	Sequence 1, Appl1	C 819	15	0.9	1406	10	US-09-745-763-18	Sequence 18, Appl
C 747	15	0.9	1095	10	US-09-898-533-8	Sequence 8, Appl1	C 820	15	0.9	1435	9	US-10-098-841-165	Sequence 165, App
C 748	15	0.9	1122	9	US-09-738-626-674	Sequence 674, App	C 821	15	0.9	1438	10	US-09-997-701-4	Sequence 4, Appl1
C 749	15	0.9	1145	10	US-09-974-300-6297	Sequence 6297, Ap	C 822	15	0.9	1452	9	US-09-954-531-147	Sequence 147, App

C 823	15	0.9	1452	5	US-09-292-758-27	Sequence 27, Appl
C 824	15	0.9	1452	10	US-09-564-456-695	Sequence 66, App
C 825	15	0.9	1452	10	US-09-954-456-1133	Sequence 1133, Ap
C 826	15	0.9	1452	10	US-09-880-107-2308	Sequence 2308, Ap
C 827	15	0.9	1452	10	US-09-957-768A-145	Sequence 145, Appl
C 828	15	0.9	1456	10	US-09-808-483-11	Sequence 2878, Ap
C 829	15	0.9	1458	10	US-09-974-300-2878	Sequence 20, Appl
C 830	15	0.9	1475	5	US-10-023-437-64	Sequence 57, Appl
C 831	15	0.9	1483	5	US-10-058-841-20	Sequence 643, Ap
C 832	15	0.9	1490	5	US-10-016-157A-57	Sequence 122, App
C 833	15	0.9	1491	10	US-09-815-242-6453	Sequence 122, App
C 834	15	0.9	1508	10	US-09-900-379-122	Sequence 2, Appl
C 835	15	0.9	1508	10	US-09-848-164-122	Sequence 8, Appl
C 836	15	0.9	1508	10	US-09-766-378A-24	Sequence 441, App
C 837	15	0.9	1512	10	US-09-335-710-1	Sequence 441, App
C 838	15	0.9	1525	5	US-10-068-841-21	Sequence 441, App
C 839	15	0.9	1545	12	US-10-033-045-5	Sequence 9, Appl
C 840	15	0.9	1557	10	US-09-804-625-1	Sequence 1, Appl
C 841	15	0.9	1570	5	US-10-098-841-236	Sequence 236, App
C 842	15	0.9	1575	5	US-09-938-842A-1623	Sequence 1623, Ap
C 843	15	0.9	1575	10	US-09-912-175-2	Sequence 2, Appl
C 844	15	0.9	1575	5	US-10-036-041-8	Sequence 8, Appl
C 845	15	0.9	1575	5	US-10-035-855-8	Sequence 8, Appl
C 846	15	0.9	1575	5	US-10-174-550-441	Sequence 441, App
C 847	15	0.9	1575	5	US-10-176-758-441	Sequence 441, App
C 848	15	0.9	1575	12	US-10-036-342-8	Sequence 8, Appl
C 849	15	0.9	1575	12	US-10-052-585-441	Sequence 441, App
C 850	15	0.9	1592	5	US-09-672-714-5	Sequence 9, Appl
C 851	15	0.9	1602	5	US-09-938-842A-857	Sequence 857, App
C 852	15	0.9	1608	10	US-09-808-483-9	Sequence 9, Appl
C 853	15	0.9	1625	10	US-09-738-626-7225	Sequence 2725, Ap
C 854	15	0.9	1632	10	US-09-938-956-6	Sequence 6, Appl
C 855	15	0.9	1635	10	US-09-880-107-2340	Sequence 2340, Ap
C 856	15	0.9	1644	10	US-09-887-586A-3	Sequence 3, Appl
C 857	15	0.9	1644	10	US-09-887-586A-5	Sequence 5, Appl
C 858	15	0.9	1644	10	US-09-887-585A-7	Sequence 7, Appl
C 859	15	0.9	1644	10	US-09-887-586A-9	Sequence 9, Appl
C 860	15	0.9	1644	10	US-09-887-586A-11	Sequence 11, Appl
C 861	15	0.9	1644	10	US-09-903-012-3	Sequence 3, Appl
C 862	15	0.9	1644	10	US-09-903-012-5	Sequence 5, Appl
C 863	15	0.9	1644	10	US-09-903-012-7	Sequence 7, Appl
C 864	15	0.9	1644	10	US-09-903-012-9	Sequence 9, Appl
C 865	15	0.9	1644	10	US-09-903-012-11	Sequence 11, Appl
C 866	15	0.9	1652	10	US-09-815-837-80	Sequence 80, Appl
C 867	15	0.9	1655	10	US-09-728-952-73	Sequence 73, Appl
C 868	15	0.9	1670	10	US-09-880-107-3833	Sequence 3833, Ap
C 869	15	0.9	1671	10	US-09-785-651-3	Sequence 3, Appl
C 870	15	0.9	1671	10	US-09-887-586A-1	Sequence 1, Appl
C 871	15	0.9	1671	10	US-09-903-012-1	Sequence 1, Appl
C 872	15	0.9	1680	10	US-09-815-837-49	Sequence 49, Appl
C 873	15	0.9	1684	5	US-09-938-842A-4070	Sequence 4070, Ap
C 874	15	0.9	1685	10	US-09-815-837-65	Sequence 65, Appl
C 875	15	0.9	1690	5	US-10-066-500-51	Sequence 51, Appl
C 876	15	0.9	1690	5	US-10-174-550-445	Sequence 445, App
C 877	15	0.9	1690	12	US-10-176-758-449	Sequence 449, App
C 878	15	0.9	1692	10	US-09-525-288-52	Sequence 52, Appl
C 879	15	0.9	1692	10	US-09-745-288-52	Sequence 9, Appl
C 880	15	0.9	1694	5	US-09-966-350-5	Sequence 79, Appl
C 881	15	0.9	1696	10	US-09-815-837-75	Sequence 62, Appl
C 882	15	0.9	1701	10	US-09-815-837-62	Sequence 62, Appl
C 883	15	0.9	1707	10	US-09-815-837-64	Sequence 64, Appl
C 884	15	0.9	1713	5	US-09-938-842A-1708	Sequence 1708, Ap
C 885	15	0.9	1728	10	US-09-925-302-239	Sequence 239, App
C 886	15	0.9	1740	5	US-09-938-842A-2315	Sequence 2315, Ap
C 887	15	0.9	1743	5	US-09-954-531-153	Sequence 153, App
C 888	15	0.9	1743	5	US-10-063-347-75	Sequence 75, Appl
C 889	15	0.9	1743	12	US-10-006-867-75	Sequence 75, Appl
C 890	15	0.9	1792	10	US-09-925-701-259	Sequence 259, Appl
C 891	15	0.9	1795	10	US-09-345-385-13	Sequence 13, Appl
C 892	15	0.9	1811	5	US-10-068-841-51	Sequence 51, Appl
C 893	15	0.9	1818	5	US-09-771-457C-3	Sequence 3, Appl
C 894	15	0.9	1855	5	US-09-965-528-43	Sequence 43, Appl
C 895	15	0.9	1858	10	US-09-835-996A-1	Sequence 1, Appl
C 896	15	0.9	1875	5	US-09-938-842A-2959	Sequence 2959, Ap
C 897	15	0.9	1875	12	US-10-081-859-1	Sequence 1, Appl
C 898	15	0.9	1875	10	US-09-935-966A-40	Sequence 40, Appl
C 899	15	0.9	1879	10	US-09-751-877-2	Sequence 40, Appl
C 900	15	0.9	1897	10	US-09-908-8055-40	Sequence 40, Appl
C 901	15	0.9	1897	10	US-09-789-561-49	Sequence 49, Appl
C 902	15	0.9	1899	10	US-09-815-242-6815	Sequence 6815, Ap
C 903	15	0.9	1900	10	US-09-973-322-4	Sequence 4, Appl
C 904	15	0.9	1901	10	US-09-925-300-632	Sequence 632, App
C 905	15	0.9	1928	10	US-09-917-800A-1332	Sequence 1332, Ap
C 906	15	0.9	1954	10	US-09-864-761-10562	Sequence 10562, A
C 907	15	0.9	1955	10	US-09-864-761-2882	Sequence 2882, Ap
C 908	15	0.9	1963	10	US-09-864-761-2897	Sequence 2897, Ap
C 909	15	0.9	1975	5	US-10-098-841-90	Sequence 90, Appl
C 910	15	0.9	1986	5	US-09-938-842A-4253	Sequence 4253, Ap
C 911	15	0.9	1988	10	US-09-764-869-1788	Sequence 1788, Ap
C 912	15	0.9	1990	10	US-09-822-845A-107	Sequence 107, App
C 913	15	0.9	1998	10	US-09-833-381-1139	Sequence 1139, Ap
C 914	15	0.9	1998	10	US-09-938-842A-2729	Sequence 2729, Ap
C 915	15	0.9	2000	5	US-09-938-842A-3304	Sequence 3304, Ap
C 916	15	0.9	2000	5	US-09-938-842A-3510	Sequence 3510, Ap
C 917	15	0.9	2000	5	US-09-938-842A-3631	Sequence 3631, Ap
C 918	15	0.9	2000	5	US-09-938-842A-3657	Sequence 3657, Ap
C 919	15	0.9	2000	5	US-09-938-842A-3701	Sequence 3701, Ap
C 920	15	0.9	2000	5	US-09-938-842A-4431	Sequence 4431, Ap
C 921	15	0.9	2000	5	US-09-938-842A-4691	Sequence 4691, Ap
C 922	15	0.9	2000	5	US-09-938-842A-4722	Sequence 4722, Ap
C 923	15	0.9	2000	10	US-09-887-576-848	Sequence 848, App
C 924	15	0.9	2028	10	US-09-840-787-73	Sequence 73, Appl
C 925	15	0.9	2030	10	US-09-925-297-71	Sequence 71, Appl
C 926	15	0.9	2053	10	US-09-815-837-63	Sequence 63, Appl
C 927	15	0.9	2059	10	US-09-815-837-66	Sequence 66, Appl
C 928	15	0.9	2071	10	US-09-799-777-118	Sequence 118, App
C 929	15	0.9	2100	10	US-09-804-626-5	Sequence 5, Appl
C 930	15	0.9	2113	10	US-09-938-803-22	Sequence 22, Appl
C 931	15	0.9	2135	5	US-09-822-830A-102	Sequence 102, App
C 932	15	0.9	2139	10	US-10-008-355-1	Sequence 1, Appl
C 933	15	0.9	2139	10	US-09-880-107-3876	Sequence 3876, Ap
C 934	15	0.9	2144	10	US-09-919-497-26	Sequence 26, App
C 935	15	0.9	2148	10	US-09-841-132-328	Sequence 328, App
C 936	15	0.9	2149	10	US-09-925-301-13	Sequence 130, Appl
C 937	15	0.9	2157	10	US-09-925-301-12	Sequence 12, Appl
C 938	15	0.9	2170	10	US-09-887-586A-21	Sequence 21, Appl
C 939	15	0.9	2170	10	US-09-903-012-21	Sequence 21, Appl
C 940	15	0.9	2181	5	US-09-938-842A-1866	Sequence 1866, Ap
C 941	15	0.9	2190	10	US-09-834-875-1031	Sequence 1031, Ap
C 942	15	0.9	2217	10	US-09-937-635-3	Sequence 3, Appl
C 943	15	0.9	2223	10	US-09-912-020-132	Sequence 132, App
C 944	15	0.9	2224	10	US-09-873-637-1	Sequence 1, Appl
C 945	15	0.9	2240	5	US-10-098-841-191	Sequence 191, Appl
C 946	15	0.9	2286	10	US-09-191-687B-3	Sequence 3, Appl
C 947	15	0.9	2300	5	US-10-098-841-190	Sequence 190, App
C 948	15	0.9	2310	10	US-09-950-510-11	Sequence 11, Appl
C 949	15	0.9	2328	5	US-09-938-842A-2679	Sequence 2679, App
C 950	15	0.9	2346	10	US-09-815-837-67	Sequence 67, Appl
C 951	15	0.9	2346	10	US-09-815-837-61	Sequence 61, Appl
C 952	15	0.9	2358	5	US-09-938-842A-1847	Sequence 1847, Ap
C 953	15	0.9	2375	10	US-09-764-864A-232	Sequence 232, App
C 954	15	0.9	2391	12	US-10-044-090-180	Sequence 180, App
C 955	15	0.9	2400	10	US-09-825-144-3	Sequence 3, Appl
C 956	15	0.9	2400	10	US-09-825-144-3	Sequence 3, Appl
C 957	15	0.9	2403	5	US-09-965-529-73	Sequence 73, Appl
C 958	15	0.9	2427	10	US-09-254-783A-2	Sequence 2, Appl
C 959	15	0.9	2427	12	US-10-152-058-2	Sequence 2, Appl
C 960	15	0.9	2435	10	US-09-823-038A-40	Sequence 40, Appl
C 961	15	0.9	2451	10	US-09-815-242-9849	Sequence 9849, Ap
C 962	15	0.9	2455	10	US-09-811-093-45	Sequence 45, Appl
C 963	15	0.9	2461	10	US-09-728-952-72	Sequence 72, Appl
C 964	15	0.9	2479	5	US-09-905-291A-27	Sequence 27, Appl
C 965	15	0.9	2479	5	US-10-066-500-114	Sequence 114, App
C 966	15	0.9	2479	5	US-09-902-853-27	Sequence 27, Appl
C 967	15	0.9	2479	5	US-09-907-824-27	Sequence 27, Appl
C 968	15	0.9	2479	5	US-09-907-841-27	Sequence 27, Appl

c 969	15	0.9	2479	9	US-09-904-011-27	Sequence 27, Appl
c 970	15	0.9	2479	9	US-10-028-072-349	Sequence 349, App
c 971	15	0.9	2479	10	US-09-909-320-27	Sequence 27, Appl
c 972	15	0.9	2479	10	US-09-909-088B-27	Sequence 27, Appl
c 973	15	0.9	2479	10	US-10-016-634A-33	Sequence 33, Appl
c 974	15	0.9	2527	10	US-09-950-510-1	Sequence 1, Appl1
c 975	15	0.9	2538	10	US-09-825-144-5	Sequence 5, Appl1
c 976	15	0.9	2538	10	US-09-825-144-5	Sequence 5, Appl1
c 977	15	0.9	2545	9	US-09-764-869-1559	Sequence 1559, Ap
c 978	15	0.9	2566	9	US-09-984-245-87	Sequence 87, Appl
c 979	15	0.9	2566	9	US-09-984-245-87	Sequence 87, Appl
c 980	15	0.9	2586	10	US-09-815-242-9990	Sequence 9990, Ap
c 981	15	0.9	2596	10	US-09-808-701-7	Sequence 7, Appl1
c 982	15	0.9	2615	9	US-10-114-590-523	Sequence 523, App
c 983	15	0.9	2615	9	US-10-176-758-523	Sequence 523, App
c 984	15	0.9	2615	12	US-10-052-586-523	Sequence 523, App
c 985	15	0.9	2631	10	US-09-815-242-6384	Sequence 6384, Ap
c 986	15	0.9	2643	10	US-09-815-242-6384	Sequence 6394, Ap
c 987	15	0.9	2661	10	US-09-801-368-179	Sequence 179, App
c 988	15	0.9	2661	10	US-09-795-691-1	Sequence 1, Appl1
c 989	15	0.9	2745	9	US-10-029-180-73	Sequence 73, Appl
c 990	15	0.9	2762	10	US-09-957-635-1	Sequence 1, Appl1
c 991	15	0.9	2775	9	US-09-908-153B-41	Sequence 41, Appl
c 992	15	0.9	2775	9	US-09-908-153B-41	Sequence 43, Appl1
c 993	15	0.9	2796	10	US-09-754-997A-3	Sequence 3, Appl1
c 994	15	0.9	2820	10	US-09-815-242-6700	Sequence 6700, Ap
c 995	15	0.9	2842	9	US-09-736-457-1800	Sequence 1800, Ap
c 996	15	0.9	2842	9	US-09-902-941-1800	Sequence 1800, Ap
c 997	15	0.9	2842	9	US-09-849-626-1800	Sequence 1800, Ap
c 998	15	0.9	2882	10	US-09-986-632-7	Sequence 653, Appl
c 999	15	0.9	2889	12	US-10-044-090-653	Sequence 18, Appl
c 1000	15	0.9	2947	9	US-09-764-868-18	

ALIGNMENTS

RESULT 1
US-09-917-265-61
Sequence 61, Application US/09917265
Patent No. US20020052030A1
GENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT: Borouhng, Karen L.
FILE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
FILE REFERENCE: IM-5
CURRENT APPLICATION NUMBER: US/09/917, 265
PRIOR FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: 60/223, 016
NUMBER OF SEQ ID NOS: 109
SOFTWARE: PatentIn version 3.1
SEQ ID NO 61
LENGTH: 1599
TYPE: DNA
ORGANISM: Canis familiaris
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1599)
OTHER INFORMATION:
US-09-917-265-61

Query Match 100.0%; Score 1599; DB 10; length 1599;
Best local similarity 100.0%; Pred. No. 0;
Matches 1599; Conservative 0; Mismatches 0; Indels 0; Caps 0;

OY 1 ATGACCCCTCAGCAGTTGGTATCTCTGTTTCCTCGTTTTCGTTGGCGCTCTCCCTC 60
DB 1 ATGACCCCTCAGCAGTTGGTATCTCTCGTTTTCCTCGTTTTCGTTGGCGCTCTCCCTC 60
OY 61 ATGACCATATGGAGCAAGGAGATGTTATGTTAGAGTTGGAGCTGGCACCCTGAT 120
DB 61 ATGACCATATGGAGCAAGGAGATGTTATGTTAGAGTTGGAGCTGGCACCCTGAT 120

OY 121 GCCCCCGAGAAATGTTGTTCTTACCTGCATACCCCTGAGAAGATGATCATCTTGG 180
DB 121 GCCCCCGAGAAATGTTGTTCTTACCTGCATACCCCTGAGAAGATGATCATCTTGG 180
OY 181 ACCTCAGCGCAGCAGCTGAAGTCTTAGTTCGTCTAAACTCTGACCATTCAGTCAA 240
DB 181 ACCTCAGCGCAGCAGCTGAAGTCTTAGTTCGTCTAAACTCTGACCATTCAGTCAA 240
OY 241 GAATTTGGAGATGCTGTCGATACCTGCATTAAGGAGCAAGTTCTGAGCCGCTCA 300
DB 241 GAATTTGGAGATGCTGTCGATACCTGCATTAAGGAGCAAGTTCTGAGCCGCTCA 300
OY 301 CTCCTGTTGATTCACAAAAGAGATGAATTTGTCACCTGATATCTTAAAGAAC 360
DB 301 CTCCTGTTGATTCACAAAAGAGATGAATTTGTCACCTGATATCTTAAAGAAC 360
OY 361 AAGCAATCCAAAATTAAGATCTTTCTGAATGTGAGGCAAGAAATTAATTCGACGTTTC 420
DB 361 AAGCAATCCAAAATTAAGATCTTTCTGAATGTGAGGCAAGAAATTAATTCGACGTTTC 420
OY 421 ACATGCTGGTGGCTGAGCGCAATGATGATTTGAATTCAGTCCAAAGATGAGA 480
DB 421 ACATGCTGGTGGCTGAGCGCAATGATGATTTGAATTCAGTCCAAAGATGAGA 480
OY 481 GCCTTCTGTACCCCAAGGGGTGACATGTGAGCAGTGCACATTTGACGAGAGAGGTC 540
DB 481 GCCTTCTGTACCCCAAGGGGTGACATGTGAGCAGTGCACATTTGACGAGAGAGGTC 540
OY 541 AGATGGACAACAGGATTTAAGAAATACACAGTGAAGTCTGAGAGGCGACGCTGC 600
DB 541 AGATGGACAACAGGATTTAAGAAATACACAGTGAAGTCTGAGAGGCGACGCTGC 600
OY 601 CCTCTGCCGAGAGACCTACCATCGAGTCTGCTGTGATCTTATCAAGCTCAAG 660
DB 601 CCTCTGCCGAGAGACCTACCATCGAGTCTGCTGTGATCTTATCAAGCTCAAG 660
OY 661 TATGAAAATTAACACACAGCTTCTTATGAGACATCATCAAAACACACCCACA 720
DB 661 TATGAAAATTAACACACAGCTTCTTATGAGACATCATCAAAACACACCCACA 720
OY 721 AACCTGACGTGAAGCCATTGAAATTTCTGCGAGCTGAGAGCTGGGAATATCCC 780
DB 721 AACCTGACGTGAAGCCATTGAAATTTCTGCGAGCTGAGAGCTGGGAATATCCC 780
OY 781 GACACCTGAGACCCCAATCTCTACTCTCCCTGACATTTTGCATACAGCCAGGC 840
DB 781 GACACCTGAGACCCCAATCTCTACTCTCCCTGACATTTTGCATACAGCCAGGC 840
OY 841 AAGACAAATAGAGAAAGAAAGATAGACTGCGTGGACAAGACTCAGCCAAAGTCTG 900
DB 841 AAGACAAATAGAGAAAGAAAGATAGACTGCGTGGACAAGACTCAGCCAAAGTCTG 900
OY 901 TGGCACAAGATGCGCAAGTCCGCTGCAAGCCGACACCGCTACTATTCATCTCTGG 960
DB 901 TGGCACAAGATGCGCAAGTCCGCTGCAAGCCGACACCGCTACTATTCATCTCTGG 960
OY 961 AGCGACTGGGCACTGTGTATGATGAGTGTGGCGGTGGCGGCGATCTAGAAACTTGGCA 1020
DB 961 AGCGACTGGGCACTGTGTATGATGAGTGTGGCGGTGGCGGCGATCTAGAAACTTGGCA 1020
OY 1021 ACCCTTACTCCATCCCGGGGTATGTTCCAAATGTTTGAACCACTCCCAACCTTGTGAGA 1080
DB 1021 ACCCTTACTCCATCCCGGGGTATGTTCCAAATGTTTGAACCACTCCCAACCTTGTGAGA 1080
OY 1081 GCCCTCAGCAACAGCTTTCAGAGAGCCAGACAAACTCTAGAAATTAATTCCTGACATTC 1140
DB 1081 GCCCTCAGCAACAGCTTTCAGAGAGCCAGACAAACTCTAGAAATTAATTCCTGACATTC 1140
OY 1141 GAAGAGATTTGATCATGAAGATATACAAAGGATTAACCCAGCAGTGGAGGCTGCTTA 1200
DB 1141 GAAGAGATTTGATCATGAAGATATACAAAGGATTAACCCAGCAGTGGAGGCTGCTTA 1200

QY	1201	GCATCGGAATTTAACCATGAACTGAGACTCCGCTGCTTCACAGAGACTCTTTGATAACT	1260
Dh	1201	CCATCTGCAATTTAACCATGAACTGAGACTCCGCTTCACAGAGACTCTTTGATAACT	1260
QY	1261	AACGGAGTTGGCTGGGCTCTGGAAGGGCTCTTTATGACGCTCTGGCTTAGACAGC	1320
Dh	1261	AACGGAGTTGGCTGGGCTCTGGAAGGGCTCTTTATGACGCTCTGGGCTTAGACAGC	1320
QY	1321	ATCTATGAGGACCTTGAAGATGTACCAAGATGGAATTCAGGGCATGACGCAAGCTTTTA	1380
Dh	1321	ATCTATGAGGACCTTGAAGATGTACCAAGATGGAATTCAGGGCATGACGCAAGCTTTTA	1380
QY	1381	ATGATCTCCCAAGACGACGATCTTTCTGATCAAAACATCTGTACAGCTATGTGATGAGCTG	1440
Dh	1381	ATGATCTCCCAAGACGACGATCTTTCTGATCAAAACATCTGTACAGCTATGTGATGAGCTG	1440
QY	1441	TTACAGCGCTCGAATTTCAACACTGTGACTGTGCGCCACGAAATCTCGCTTGAAAGAGCGG	1500
Dh	1441	TTACAGCGCTCGAATTTCAACACTGTGACTGTGCGCCACGAAATCTCGCTTGAAAGAGCGG	1500
Y	1501	GATTTTATTAACACTAAAAATCAAGCTCTGCTATACCTCTTTCATAGCTTTTCAGAAATTCGTGGC	1560
Dh	1501	GATTTTATTAACACTAAAAATCAAGCTCTGCTATACCTCTTTCATAGCTTTTCAGAAATTCGTGGC	1560
QY	1561	GTGAGCATCAATTAATGATGTCTTACTGTGAACCTCTTCC	1599
Dh	1561	GTGAGCATCAATTAATGATGTCTTACTGTGAACCTCTTTCG	1599

RESULT 2

US-09-917-265--63/c
Sequence 63, Application US/09917265
Patent No. US20020052030A1
GENERAL INFORMATION:
APPLICANT: Wonderling, Remani S.
APPLICANT: Borouhbs, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
FILE REFERENCE: IN-5
CURRENT APPLICATION NUMBER: US/09/917,265
CURRENT FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ. ID NOS: 109
SOFTWARE: patentIn version 3.1
SEQ. ID NO. 63
LENGTH: 1559
TYPE: DNA
ORGANISM: Canis familiaris
S-09-917-265--63

Query Match 100.0%; Score 1599; DB 10; Length 1599;

Best Local Similarity: 100.0%; Pred. NO. 0;
Matches 1555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGACCCCTCAGCAGAGTTGATCATCTCCCTGGTTTCCTGCTGGCCCTCCCTC	60
Dh	1599	ATGACGCCCTCAGCAAGTTGGTCACTCTCCCTGGTTTTCCTGCTGGCCCTCCCTC	1540
QY	61	ATGGCCCATATGGCAACTCGAGAAGATGTTTATGTTGTAGAGTTGCACTGGACCCCTGAT	120
Dh	1539	ATGGCCCATATGGCAACCTCGAGAAGATGTTTATGTTGTAGAGTTGCACTGGACCCCTGAT	1480
QY	121	GGCCCGCGAAGAAATGGTGTGCTCTCACCTCTCCATACCCCTCGAAGAAGATGACATCACTTGG	180
Dh	1479	GGCCCGCGAAGAAATGGTGTGCTCTCACCTCTCCATACCCCTCGAAGAAGATGACATCACTTGG	1420
QY	181	ACCTCACCAGTAGGAGCGAGTAAATGCTTAGGTTTGTTAAAACTCTGACATCGAATGATAAA	240
Dh	1419	ACCTCACCAGTAGGAGCGAGTGAAGTCTTAGGTTTGTTAAAACTCTGACATCGAATGATAAA	1360
QY	241	GAATTTCGATATGCTCTGACGAGTATACCTCCGATAAAGAGCGTAGGTTCTGAGCGCTCA	300
Dh	1359	GAATTTCGATATGCTGAGCAAGTATACCTCCGATAAAGAGCGTAGGTTCTGAGCGCTCA	1300

QY	301	CTCCGTGTTGATTTCACAAAAAGAAAGATGGAATTTGGTCCACATGATATCTTAAAGAACAG	360
DB	1299	CTCCGTGTTGATTTCACAAAAAGAAAGATGGAATTTGGTCCACATGATATCTTAAAGAACAG	1240
QY	361	AAAGAATTCAAAAATTAAGATCTTTCTGAAATGTGACGCACAAGAATTTATTCTGACGTTTC	420
DB	1239	AAAGAATTCAAAAATTAAGATCTTTCTGAAATGTGACGCACAAGAATTTATTCTGACGTTTC	1180
QY	421	ACATGCTGTGGGCTGACGGGCATCAGACGTGATTTGAAATTCAGTGTCAAAAGTAGCAGA	480
DB	1179	ACATGCTGTGGGCTGACGGGCATCAGACGTGATTTGAAATTCAGTGTCAAAAGTAGCAGA	1120
QY	481	GCGTTCTCTGACCCCTCAAGGGGTGACATGTGAGCAGTCACACTTTCAGCAGAGAGGCTC	540
DB	1119	GCGTTCTCTGACCCCTCAAGGGGTGACATGTGAGCAGTCACACTTTCAGCAGAGAGGCTC	1060
QY	541	AGAAGTGACAAACAGGAGATTATTAAGAAGTACACAGTGGAGTGTACGAGAGGCAGTCCCTGC	600
DB	1059	AGAAGTGACAAACAGGAGATTATTAAGAAGTACACAGTGGAGTGTACGAGAGGCAGTCCCTGC	1000
QY	601	CCCTCTCTCCGAGGAGACCTTACCCATTCGAGGTGTGGTGGATGTATTCACAGCTCAAG	660
DB	999	CCCTCTCTCCGAGGAGACCTTACCCATTCGAGGTGTGGTGGATGTATTCACAGCTCAAG	940
QY	661	TATGAAACCTACACCTACAGCTTCTTCATCAGAGCATCATCAAAACAGCCACCACGA	720
DB	939	TATGAAACCTACACCTACAGCTTCTTCATCAGAGCATCATCAAAACAGCCACCACGA	880
QY	721	AACTGTCAGCTGAAGCCATTGAAAAAATTTCTCGGACAGTGGAGGTGAGCTGGGAAATACCC	780
DB	879	AACTGTCAGCTGAAGCCATTGAAAAAATTTCTCGGACAGTGGAGGTGAGCTGGGAAATACCC	820
QY	781	GACACCTGTGAGACACCCCAACATCTCTACTCTCTCCCTACATTTTGCATACAGGCCAGAGGC	840
DB	819	GACACCTGTGAGACACCCCAACATCTCTACTCTCTCCCTACATTTTGCATACAGGCCAGAGGC	760
QY	841	AAGAACAATTACGAAAAAGAAAGATAGACCTGTGCTGGACACAGACCTCAAGCTGCTG	900
DB	759	AAGAACAATTACGAAAAAGAAAGATAGACCTGTGCTGGACACAGACCTCAAGCTGCTG	700
QY	901	TGCGACAAGATGCGCAAGATCCGCGTGCACAGCCCGAGACCGCTACTATTAGTTACATCTCGG	960
DB	699	TGCGACAAGATGCGCAAGATCCGCGTGCACAGCCCGAGACCGCTACTATTAGTTACATCTCGG	640
QY	961	AGCGCATGTGGCATCTGTGTGTATCATGCACTGTGTGGCGGTGGCGGAGTATGAAACTTGCCA	1020
DB	639	AGCGCATGTGGCATCTGTGTGTATCATGCACTGTGTGGCGGTGGCGGAGTATGAAACTTGCCA	580
QY	1021	AGCCCTACTTCCATCCCGCGGGATGTGCCAATGTTTAAACACGCCCAAACTCTGTGTGGA	1080
DB	579	AGCCCTACTTCCATCCCGCGGGATGTGTGCCAATGTTTAAACACGCCCAAACTCTGTGTGGA	520
QY	1081	GCCGTCAGACAACGCTTTCAGAAAGGCCAGACAACCTCTGAATTTATTCTCGCACTTCC	1140
DB	519	GCCGTCAGACAACGCTTTCAGAAAGGCCAGACAACCTCTGAATTTATTCTCGCACTTCC	460
QY	1141	GAAAGAGATTGATCATYGAAGATTATCACAAAGGATAAAACAGCACAGTGGAGGCCCTGTTA	1200
DB	459	GAAAGAGATTGATCATYGAAGATTATCACAAAGGATAAAACAGCACAGTGGAGGCCCTGTTA	400
QY	1201	CCACTGGAATTAAACCATGATGAGAGTGTGGCTGTGGCTTCCAGAGACATCTCTTTGATTA	1260
DB	399	CCACTGGAATTAAACCATGATGAGAGTGTGGCTGTGGCTTCCAGAGACATCTCTTTGATTA	340
QY	1261	AACGGGAGTTGCGCTGCGCTCTGGAAGAGGCCTCTTTTATCACGGTCTGTGCTTAAGCAGC	1320
DB	339	AACGGGAGTTGCGCTGCGCTCTGGAAGAGGCCTCTTTTATCACGGTCTGTGCTTAAGCAGC	280
QY	1321	ATTCTATGAGGACTTGAAGATGTACCAATGGAATTCGAAGGCCATGACGCAAAACCTTTTA	1380
DB	279	ATTCTATGAGGACTTGAAGATGTACCAATGGAATTCGAAGGCCATGACGCAAAACCTTTTA	220

QY 1381 ATGATCCCAAGAGCAGATCTTCTGGATCAAAACATGCTGACAGCTATGATGAGCTG 1440
DB 219 ATGATCCCAAGAGCAGATCTTCTGGATCAAAACATGCTGACAGCTATGATGAGCTG 160
QY 1441 TTACAGGCCCTTAATTTTCAACAGTGTGACTGTGCCACAGAAATCTCTTCAAGAGCCG 1500
DB 159 TTACAGGCCCTTAATTTTCAACAGTGTGACTGTGCCACAGAAATCTCTTCAAGAGCCG 100
QY 1501 GATTTTAAACATCAAAATCAAGCTGACATCTTTCATGCTTTTCAAGATTTGGTGG 1560
DB 99 GATTTTAAACATCAAAATCAAGCTGTGCATCTTCTTCAATGCTTTTCAAGATTTGGTGG 40
QY 1561 GTGACCATCAATAGATGATGTCTACTTGAACCTCTCC 1599
DB 39 GTGACCATCAATAGATGATGTCTACTTGAACCTCTCC 1

RESULT 3
US-09-917-265-66
Sequence 66, Application US/09917265
Patent No. US20020052030A1

GENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT: Broughs, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
FILE REFERENCE: IM-5
CURRENT APPLICATION NUMBER: US/09/917,265
PRIORITY FILING DATE: 2001-07-27
PRIORITY FILING DATE: 2000-08-04
PRIORITY FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 109
SOFTWARE: Patentin version 3.1
SEQ ID NO 66
LENGTH: 1533
TYPE: DNA
ORGANISM: Canis familiaris
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1533)
OTHER INFORMATION:
US-09-917-265-66

Query Match 95.9%; Score 1533; DB 10; Length 1533;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1533; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 ATATGGGAACCTGGAAAGATCTTTATGTGTGAGAGTTGGAGCTGGCACCCTGATGCCCC 126
1 ATATGGGAACCTGGAAAGATGTATTATGTGTGAGAGTTGGAGCTGGCACCCTGATGCCCC 60
QY 127 GGAGAAATGCTGCTCCTACCTGCCATACCCCTGAAGAAGATGATGATGAGCTCA 186
DB 61 GGAGAAATGCTGCTCCTACCTGCCATACCCCTGAAGAAGATGATGATGAGCTCA 120
QY 187 GCGCAGACAGTGAAGTCTTGTGTAAGTCTGACCATCAAGTCAAGAAATTT 246
DB 121 GCGCAGACAGTGAAGTCTTGTGTAAGTCTGACCATCAAGTCAAGAAATTT 180
QY 247 GGAGATGCTGGCAGTATACCGCCATAAAGGAGGCAAGTCTTGAAGCCGCTACCTCG 306
DB 181 GGAGATGCTGGCAGTATACCGCCATAAAGGAGGCAAGTCTTGAAGCCGCTACCTCG 240
QY 307 TTGATTCACAAAAGAAAGATGGAATTTGTCACACTGATATCTTAAAGACAGAAAGAA 366
DB 241 TTGATTCACAAAAGAAAGATGGAATTTGTCACACTGATATCTTAAAGACAGAAAGAA 300
QY 367 TCACAAAATTAAGATCTTTCTGTAATGTAGGCAAGAAATTAATCTTGAAGCTTTCACATGC 426
DB 301 TCACAAAATTAAGATCTTTCTGTAATGTAGGCAAGAAATTAATCTTGAAGCTTTCACATGC 360
QY 427 TGGGGCTGAGGCGCAATGATGATGATTTGAAATTCATGTCTCAAAAGTACAGAGGCTTC 486
DB 361 TGGGGCTGAGGCGCAATGATGATGATTTGAAATTCATGTCTCAAAAGTACAGAGGCTTC 420

QY 487 TCTGACCCCAAGGGGTGACATGTGACAGTGAACCTTTTCAGAGAGGGGTGAGAGT 546
DB 421 TCTGACCCCAAGGGGTGACATGTGACAGTGAACCTTTTCAGAGAGGGGTGAGAGT 480
QY 547 GACAACAGGGAATTAAGAAGTACACAGTGTGAGTGTGAGAGGAGGAGTGTGAGAGT 606
DB 481 GACAACAGGGAATTAAGAAGTACACAGTGTGAGTGTGAGAGGAGGAGTGTGAGAGT 540
QY 607 GCCGAGAGAGGCTTACCATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 666
DB 541 GCCGAGAGAGGCTTACCATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 600
QY 667 AACTACACAGAGCTTCTTCTGAGAGACATCAACCAAGGAGGAGGAGGAGGAGGAGGAG 726
DB 601 AACTACACAGAGCTTCTTCTGAGAGACATCAACCAAGGAGGAGGAGGAGGAGGAGGAG 660
QY 727 CAGCTGAAGCCATTTGAAAATTTCTGGGACGCTGAGAGTGTGAGTGTGAGTGTGAGTGTGAG 786
DB 661 CAGCTGAAGCCATTTGAAAATTTCTGGGACGCTGAGAGTGTGAGTGTGAGTGTGAGTGTGAG 720
QY 787 TGGAGACCCCAATCTTCTTCTGAGATTTTGTGATTTTGTGATTTTGTGATTTTGTGATTTTGTGAT 846
DB 721 TGGAGACCCCAATCTTCTTCTGAGATTTTGTGATTTTGTGATTTTGTGATTTTGTGATTTTGTGAT 780
QY 847 AATAGAGAAAGAAAGATAGACTGTGCTGAGAGACCTGAGAGGAGGAGGAGGAGGAGGAGGAG 906
DB 781 AATAGAGAAAGAAAGATAGACTGTGCTGAGAGACCTGAGAGGAGGAGGAGGAGGAGGAGGAG 840
QY 907 AAGATGCGCAAGATCGGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 966
DB 841 AAGATGCGCAAGATCGGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
QY 967 TGGGATCTGTGTGATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1026
DB 901 TGGGATCTGTGTGATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 960
QY 1027 ACTCCATCCCGGGGTATGCTTCCCAATGTTTGAACCACTCCCAAACTTTTGAAGAGCCGTC 1086
DB 961 ACTCCATCCCGGGGTATGCTTCCCAATGTTTGAACCACTCCCAAACTTTTGAAGAGCCGTC 1020
QY 1087 AGCAACAGCCTTTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1146
DB 1021 AGCAACAGCCTTTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080
QY 1147 ATTGATCATGAAGATATGCAAAAGATTAACACAGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAG 1206
DB 1081 ATTGATCATGAAGATATGCAAAAGATTAACACAGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140
QY 1207 GAATTAACCATGAATGAGAGTGTGCTGCTTCCAGAGAGATCTTTGATTAACCTAACGGG 1266
DB 1141 GAATTAACCATGAATGAGAGTGTGCTGCTTCCAGAGAGATCTTTGATTAACCTAACGGG 1200
QY 1267 AGTTCCTGCGCTCTGGAAGAGGCTCTTTTATGACGCTGCTGCTTATGACAGATCTAT 1326
DB 1201 AGTTCCTGCGCTCTGGAAGAGGCTCTTTTATGACGCTGCTGCTTATGACAGATCTAT 1260
QY 1327 GAGGACTTGAAGATGTACAGATGGAATTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1386
DB 1261 GAGGACTTGAAGATGTACAGATGGAATTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1320
QY 1387 CCCAAGAGGAGATCTTTCTGATCAAAAACATGCTGACAGGATGATGATGATGATGATGATGATGATGAT 1446
DB 1321 CCCAAGAGGAGATCTTTCTGATCAAAAACATGCTGACAGGATGATGATGATGATGATGATGATGATGAT 1380
QY 1447 GCCCTGAATTTCAACAGTGTGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1506
DB 1381 GCCCTGAATTTCAACAGTGTGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1440
QY 1507 TATTAACCTAAATCAACCTGCTGATCTTCTGATGCTTCTGATGCTTCTGATGCTTCTGATGCTTCTGAT 1566
DB 1441 TATTAACCTAAATCAACCTGCTGATCTTCTGATGCTTCTGATGCTTCTGATGCTTCTGATGCTTCTGAT 1500


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QY 1567 ATCAATAGATGATGCTCTACTGAACTCTTCC 1599
Db 1501 ATCAATAGATGATGCTCTACTGAACTCTTCC 1533

RESULT 4
US-09-917-265-68/c
: Sequence 68, Application US/09917265
: Patent No. US20020052030A1
: GENERAL INFORMATION:
: APPLICANT: Wonderling, Ramani S.
: APPLICANT: Boroughs, Karen L.
: TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
: FILE REFERENCE: IM-5
: CURRENT APPLICATION NUMBER: US/09/917,265
: CURRENT FILING DATE: 2001-07-27
: PRIOR APPLICATION NUMBER: 60/223,016
: PRIOR FILING DATE: 2000-08-04
: NUMBER OF SEQ ID NOS: 105
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 68
: LENGTH: 1533
: TYPE: DNA
: ORGANISM: Canis familiaris
: US-09-917-265-68

Query Match 95.9% Score 1533: DB 10: Length 1533:
Best Local Similarity 100.0%: Pred. No. 0:
Matches 1533: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 67 ATATGGAACTGGAGAAAGATGTTATGTTAGAGTGGACCTGGACCTGATGCCCC 126
Db 1533 ATATGGAACTGGAGAAAGATGTTATGTTAGAGTGGACCTGGACCTGATGCCCC 1474

QY 127 GGAGAAATGCTGCTCTACCTGCCATAGCCCTGAGAGACATGATCATTGGACCTCA 186
Db 1473 GGAGAAATGCTGCTCTACCTGCCATAGCCCTGAGAGACATGATCATTGGACCTCA 1414

QY 187 GCGGAGAGCACTGAAGCTCTAGGTTCTGTAAAGCTGACATCCAGTCGAAGAATTT 246
Db 1413 GCGGAGAGCACTGAAGCTCTAGGTTCTGTAAAGCTGACATCCAGTCGAAGAATTT 1354

QY 247 GGAGATGCTGGCCAGTATACCTGCCATTAAGCAGGCAAGCTTCTGAGCCCTCACTCTG 306
Db 1353 GGAGATGCTGGCCAGTATACCTGCCATTAAGCAGGCAAGCTTCTGAGCCCTCACTCTG 1294

QY 307 TTGATTCACAAAAGAAAGATGGAATTTGGTCCACTGATATCTTAAGGAAGAAAGAA 366
: 1293 TTGATTCACAAAAGAAAGATGGAATTTGGTCCACTGATATCTTAAGGAAGAAAGAA 1234

QY 367 TGCAAAATATAGATCTTCTGTAATCTGAGGCAAAAGATTTCTGGACGTTTCACATGC 426
Db 1233 TGCAAAATATAGATCTTCTGTAATCTGAGGCAAAAGATTTCTGGACGTTTCACATGC 1174

QY 427 TGTGTGCTGAGCGCAATCAGTACTGATTTGAATTTCACTGTCAAAAGTAGCAGAGCTTC 486
Db 1173 TGTGTGCTGAGCGCAATCAGTACTGATTTGAATTTCACTGTCAAAAGTAGCAGAGCTTC 1114

QY 487 TGTGACCCCTTAAGGCTGACATGTGAGCAGACTTTCAGCAGAGAGGCTCAGAGCTG 546
Db 1113 TGTGACCCCTTAAGGCTGACATGTGAGCAGACTTTCAGCAGAGAGGCTCAGAGCTG 1054

QY 547 GACAAAGAGGATTTATAAAGCTACAGATGAGTGTGAGGAGGAGGCTGGCCCTCT 606
Db 1053 GACAAAGAGGATTTATAAAGCTACAGATGAGTGTGAGGAGGAGGCTGGCCCTCT 994

QY 607 GCGGAGAGAGAGCTTACCTATCAGAGGCTCTGTGTGATGCTATTTCACAAAGCTTAAGTAGAA 666
Db 993 GCGGAGAGAGAGCTTACCTATCAGAGGCTCTGTGTGATGCTATTTCACAAAGCTTAAGTAGAA 534

QY 667 AACACAGCAGCTAGCTTTCTCATCAGAGACATCATCAAGCAGAGCCAGCCAGCAAGCTG 726
Db 933 AACACAGCAGCTAGCTTTCTCATCAGAGACATCATCAAGCAGAGCCAGCCAGCAAGCTG 874
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QY 727 CAGCTGAAGCCATTGAAAAATTTCTGGCAGGNGAGAGCTCAGCTGGGAATACCCGACAC 786
Db 873 CAGCTGAAGCCATTGAAAAATTTCTGGCAGGNGAGAGCTCAGCTGGGAATACCCGACAC 814

QY 787 TGAACACACCCACATCTCTACTTCTCCCTGACATTTTGCATACAGGCCCAGAGGCAAGAC 846
Db 813 TGAACACACCCACATCTCTACTTCTCCCTGACATTTTGCATACAGGCCCAGAGGCAAGAC 754

QY 847 AATAGAGAAAGAAAGATAGACTCTGCGTGGACAGAACCTCAGCCAGCTGCTGCGCAC 906
Db 753 AATAGAGAAAGAAAGATAGACTCTGCGTGGACAGAACCTCAGCCAGCTGCTGCGCAC 694

QY 907 AAGATGGCAAGATCCGGGTGCAACCCGACAGCCGCTACTATAGTCAATCTCGAGCGAC 966
Db 693 AAGATGGCAAGATCCGGGTGCAACCCGACAGCCGCTACTATAGTCAATCTCGAGCGAC 634

QY 967 TGGGATCTGTCTCATGACAGTGGTGGCGGTGGCGGATCTAGAAACTTGGCAACCCCT 1026
Db 633 TGGGATCTGTCTCATGACAGTGGTGGCGGTGGCGGATCTAGAAACTTGGCAACCCCT 574

QY 1027 ACTCCATCCCGGGGTATGTTCCATGTTTGAACCACTCCAAACCTTTGAGAACCGCTC 1086
Db 573 ACTCCATCCCGGGGTATGTTCCATGTTTGAACCACTCCAAACCTTTGAGAACCGCTC 514

QY 1087 AGCAACACGCTTTCAGAACGCCAGCAAACTCTAGAAATATATTCCTGACTTCCGAGAG 1146
Db 513 AGCAACACGCTTTCAGAACGCCAGCAAACTCTAGAAATATATTCCTGACTTCCGAGAG 454

QY 1147 ATTGATCATGAAGATATATACAAAGATTAACACACACAGTGGAGGCCCTGTTACCACTG 1206
Db 453 ATTGATCATGAAGATATATACAAAGATTAACACACACAGTGGAGGCCCTGTTACCACTG 394

QY 1207 GAATTAACCATGAATGAGAGTTCCTGCTTCAGAGAGATCTCTTTGATTAAGTAACGGG 1266
Db 393 GAATTAACCATGAATGAGAGTTCCTGCTTCAGAGAGATCTCTTTGATTAAGTAACGGG 334

QY 1267 AGTTGCCCTGGGCTCTGGAAGGCCCTTTTATAGACGGTCCGTGGCTTAGAGGATCTAT 1326
Db 333 AGTTGCCCTGGGCTCTGGAAGGCCCTTTTATAGACGGTCCGTGGCTTAGAGGATCTAT 274

QY 1327 GAGGACTTGAAGATCTACACATGGAATTTCAAGGCCATGAGCGCAAACTTTTATGAT 1386
Db 273 GAGGACTTGAAGATCTACACATGGAATTTCAAGGCCATGAGCGCAAACTTTTATGAT 214

QY 1387 CCCAAGAGGCAAGATCTTTCTGGAATCAAAACATGCTGACAGCTATGATGAGCTGTTACAG 1446
Db 213 CCCAAGAGGCAAGATCTTTCTGGAATCAAAACATGCTGACAGCTATGATGAGCTGTTACAG 154

QY 1447 GCGCTGAATTTCAACAGTGTGACGTGTGCAAGAAATCTCCCTTGAAGAGCCGGAATTT 1506
Db 153 GCGCTGAATTTCAACAGTGTGACGTGTGCAAGAAATCTCCCTTGAAGAGCCGGAATTT 94

QY 1507 TATAAACTAAATCAACCTCTGCACTACTTCTTATGCTTTTCAGAAATTCGTGGCGTAGC 1566
Db 93 TATAAACTAAATCAACCTCTGCACTACTTCTTATGCTTTTCAGAAATTCGTGGCGTAGC 34

QY 1567 ATCAATAGATGATGCTCTACTGAACTCTTCC 1599
Db 33 ATCAATAGATGATGCTCTACTGAACTCTTCC 3

RESULT 5
US-09-917-265-58
: Sequence 58, Application US/09917265
: Patent No. US20020052030A1
: GENERAL INFORMATION:
: APPLICANT: Wonderling, Ramani S.
: APPLICANT: Boroughs, Karen L.
: TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
: CURRENT APPLICATION NUMBER: US/09/917,265
: CURRENT FILING DATE: 2001-07-27
```

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: PRIOR APPLICATION NUMBER: 60/223,016
: PRIOR FILING DATE: 2000-08-04
: NUMBER OF SEQ ID NOS: 109
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 58
: LENGTH: 987
: TYPE: DNA
: ORGANISM: Canis familiaris
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)..(987)
: OTHER INFORMATION:
: IS-09-917-265-58

```

Query Match	61.7%	Score 987	DB 10	Length 987
Best Local Similarity	100.0%	Pred. No.	0	
Matches 987	Conservative	0	Mismatches	0
			Indels	0
			Gaps	0

QY	1	ATTACCCCTGACGAGTGGTGCATCTCCGTGGTTTTCCCTGTTTTGGCTGGGCTCTCCCTC	60
	1	ATGACACCCCTACGCACTGGTGCATCTCCGTGGTTTTCCCTGTTTTGGCTGGGCTCTCCCTC	60
OY	61	ATGGCCATATATGGGAACCTGGAGAAAGATGTTATGTGTAGAGTTGGACCTGGACCCGAT	120
Db	61	ATGGCCATATATGGGAACCTGGAGAAAGATGTTATGTGTAGAGTTGGACCTGGACCCGAT	120
OY	121	GGCCCCGGAGAAATGTGTGTCCTACCTGCCATATCCCTGAAGAAGATGACATCACTTGG	180
Db	121	GGCCCCGGAGAAATGTGTGTCCTACCTGCCATATCCCTGAAGAAGATGACATCACTTGG	180
OY	181	ACCTCAGGGCGAGACAGTGAAGTCTTGGTTCTGGTTAAACTGTGACATTCACAAGTCAA	240
Db	181	ACCTCAGGGCGAGACAGTGAAGTCTTGGTTCTGGTTAAACTGTGACATTCACAAGTCAA	240
OY	241	GAATTTGAGAGATGCTGGCCAGTATACCTGCCATTAAGGAGGCAAGTTCTGAGCCGCTCA	300
Db	241	GAATTTGAGAGATGCTGGCCAGTATACCTGCCATTAAGGAGGCAAGTTCTGAGCCGCTCA	300
OY	301	CTCCTGTGTGATTCCACAAAAAAGAAATGTGAATTTGGTCCACTGATATCTTAAAGAACAG	360
Db	301	CTCCTGTGTGATTCCACAAAAAAGAAATGTGAATTTGGTCCACTGATATCTTAAAGAACAG	360
OY	361	AAACAATCCAAAATAATAGATCTTCTGAAATGTGAGGCAAAAGATTAATCTGAGCGTTTC	420
Db	361	AAACAATCCAAAATAATAGATCTTCTGAAATGTGAGGCAAAAGATTAATCTGAGCGTTTC	420
OY	421	ACATGCTGTGGTGGCTGGACGGCAATCAGTACTGATTTGAAATTCAGTGTCCAAAAGTAGCAGA	480
Db	421	ACATGCTGTGGTGGCTGGACGGCAATCAGTACTGATTTGAAATTCAGTGTCCAAAAGTAGCAGA	480
OY	481	GGCTTCTGTGACCCCCCAAGGGGTACATGTGGACACATTCACACTTCCTGAGAGAGGGTTC	540
Db	481	GGCTTCTGTGACCCCCCAAGGGGTACATGTGGACACATTCACACTTCCTGAGAGAGGGTTC	540
OY	541	AGAGTGGACAACAGGAGATTATAGAAGCTACACAOTGAGAGTGCAGAGGGCGAGTGCCTGC	600
Db	541	AGAGTGGACAACAGGAGATTATAGAAGCTACACAOTGAGAGTGCAGAGGGCGAGTGCCTGC	600
OY	601	CCCTCTGCCGAGGAGAGCCTTACCCATGTGAGGTGTGGTGATGCTATTCCAAAGCTCAAG	660
Db	601	CCCTCTGCCGAGGAGAGCCTTACCCATGTGAGGTGTGGTGATGCTATTCCAAAGCTCAAG	660
OY	661	TATGAAGAAGTACACACAGAGTTCTTCATGAGACATCATCAAAACCCAGACCCACCCACA	720
Db	661	TATGAAGAAGTACACACAGAGTTCTTCATGAGACATCATCAAAACCCAGACCCACCCACA	720
OY	721	AACCTGAGCTGGAAGCCATTGAAAAAATTCCTGCGACGTGAGAGCTCAGCTGGGAATACCC	780
Db	721	AACCTGAGCTGGAAGCCATTGAAAAAATTCCTGCGACGTGAGAGCTCAGCTGGGAATACCC	780
OY	781	GACACCTGGAGACCCACCATTCCTACTTCTCCCTGCACATTTTGGCATACAGGCCACAGGGC	840
Db	781	GACACCTGGAGACCCACCATTCCTACTTCTCCCTGCACATTTTGGCATACAGGCCACAGGGC	840

QY	841	AAGAACATAGAGAAAGAAAGATAGACTTCTCGTGGCAAGACCTAGCCAAAGTGTG	900
Db	841	AAGAACATAGAGAAAGAAAGATAGACTTCTCGTGGCAAGACCTAGCCAAAGTGTG	900
QY	901	TGCCCAAGGATGCCAAGATCCGGGTGCAACCCGAGACCGCTACTAGTTCAATCCTGG	960
Db	901	TGCCCAAGGATGCCAAGATCCGGGTGCAACCCGAGACCGCTACTAGTTCAATCCTGG	960
QY	961	AGCGACTGGGCATCTGTCTATGGAGT	987
Db	961	AGCGACTGGGCATCTGTCTATGGAGT	987

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: RESULT 6
: US-09-917-265-60/c
: Sequence 60, Application US/09917265
: Patent No. US20020052030A1
: GENERAL INFORMATION:
: APPLICANT: Wonderling, Ramani S.
: TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
: FILE REFERENCE: 1M-5
: CURRENT APPLICATION NUMBER: US/09/917,265
: CURRENT FILING DATE: 2001-07-27
: PRIOR APPLICATION NUMBER: 60/223,016
: PRIOR FILING DATE: 2000-08-04
: NUMBER OF SEQ ID NOS: 109
: SOFTWARE: Patentin version 3.1
: SEQ ID NO 60
: LENGTH: 987
: TYPE: DNA
: ORGANISM: Canis familiaris
: US-09-917-265-60

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Query Match	61.7%	Score 987	DB 10	Length 987
Best Local Similarity	100.0%	Pred. No. 0		
Matches 987, Conservative	0	Mismatches	0	Gaps 0

Oy	1	ATGACCCCTGACAGATGGTGTATCTCTCGGTGTTTCCTCGTTTGTGGCGTCTCCCTC	60
Db	987	ATGCACCCCTGACAGATGGTGTATCTCTCGGTGTTTCCTCGTTTGTGGCGTCTCCCTC	9 28
Oy	61	ATGGCATATGGGAACCTGGAGAAGATGTATATGTGTAGAGTTGGACCTGGACCCGAT	1 20
Db	927	ATGGCATATGGGAACCTGGAGAAGATGTATATGTGTAGAGTTGGACCTGGACCCGAT	8 68
Oy	121	GCCCCCGAGAAATGTGTGTCCTGCACCTGCCATACCCCTGAGAAGATGATCACTTGG	1 80
Db	867	GCCCCCGAGAAATGTGTGTCCTGCACCTGCCATACCCCTGAGAAGATGATCACTTGG	8 08
Oy	181	ACCTCAGCGGACACAGTGAAGTCCTAGTTCCTGTAAACTGTGACCATTCGAAGTCAA	2 40
Db	807	ACCTCAGCGGACACAGTGAAGTCCTAGTTCCTGTAAACTGTGACCATTCGAAGTCAA	7 88
Oy	241	GAATTTGGAGATGCTGTGGCCATATACCTGCCATTAAGGAGCGAAGTTGTGACCCGCTCA	3 00
Db	747	GAATTTGGAGATGCTGTGGCCATATACCTGCCATTAAGGAGCGAAGTTGTGACCCGCTCA	6 88
Oy	301	CTCCGTGTGATTCAACAAAAAGAAAGATGGAATTTTGGTCCACTGATATCTTAAAGGAACAG	3 60
Db	687	CTCCGTGTGATTCAACAAAAAGAAAGATGGAATTTTGGTCCACTGATATCTTAAAGGAACAG	6 28
Oy	361	AAAGATTCACAAAATTAAGATCTTTTCTGAATGTGAGCCAAAGATTAATTCTGGACGTTTC	4 20
Db	627	AAAGATTCACAAAATTAAGATCTTTTCTGAATGTGAGCCAAAGATTAATTCTGGACGTTTC	5 68
Oy	421	ACATGCTGTGGGCGTGAAGGCAATGAGTACGATTTGGAATTTTCAGTGCACAAAGATGACGA	4 80
Db	567	ACATGCTGTGGGCGTGAAGGCAATGAGTACGATTTGGAATTTTCAGTGCACAAAGATGACGA	5 08
Oy	481	GGCTTCTCTGACCCCGAAGGGGTGACATGTGTGAGCACTGACACTTTCACGAGAGGGTC	5 40

[illegible]

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RESULT 8
US-09-917-265-109/c
: Sequence 109, Application US/09917265
: Patent No. US20020052030A1
: GENERAL INFORMATION:
: APPLICANT: Wonderling, Ramani S.
: APPLICANT: Boroughs, Karen L.
: TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
: FILE REFERENCE: IM-5
: CURRENT APPLICATION NUMBER: US/09/917,265
: CURRENT FILING DATE: 2001-07-27
: PRIOR APPLICATION NUMBER: 60/223,016
: PRIOR FILING DATE: 2000-08-04
:

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; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 109
; LENGTH: 2267
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-917-265-109
```

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Query Match          60.9%; Score 974; DB 10; Length 2267;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 974; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 7 CCTGAGCAGTTGGTCATCTCTGCTGTTTCCCTGCTTTTCTGCGGCTCTCCCTCATGAGCC 66
    |||
Db 2108 CCTGAGCAGTTGGTCATCTCTGCTGTTTCCCTGCTTTTGGCGGCTCTCCCTCATGAGCC 2049

OY 67 ATATGGGAGCTGGAGAAAGATGTTTATGTGTGTAGATTGGAGCTGGACCCCGATGCCCCC 126
    |||
Db 2048 ATATGGGAGCTGGAGAAAGATGTTTATGTGTGTAGATTGGAGCTGGACCCCGATGCCCCC 1989

    127 GGAGAAATGCTGTCTCTACCTGCCATACCCCTGAGAGAGATGACATCACTTTGGACCTCA 186
    |||
Db 1988 GGAGAAATGCTGTCTCTACCTGCCATACCCCTGAGAGAGATGACATCACTTTGGACCTCA 1929

OY 187 GCGCAGAGCAGTGAAGTCTAGTTTGTGTAAACTCTGACCATCCAAAGTCAAAAGATT 246
    |||
Db 1928 GCGCAGAGCAGTGAAGTCTAGTTTGTGTAAACTCTGACCATCCAAAGTCAAAAGATT 1869

OY 247 GGAGATCTGGCCGAGTATACCTGCTATAAAGAGAGCAAGGTTCTGAGCCGCTCACTCTG 306
    |||
Db 1868 GGAGATCTGGCCGAGTATACCTGCTATAAAGAGAGCAAGGTTCTGAGCCGCTCACTCTG 1809

OY 307 TTGATTGACAAAAAAGAGATGAATTTGTCTCAGTATATCTTAAAGAAACAGAAAGAA 366
    |||
Db 1808 TTGATTGACAAAAAAGAGATGAATTTGTCTCAGTATATCTTAAAGAAACAGAAAGAA 1749

OY 367 TCCAAAAAATAAGATCTTTTGTGAATGTGAGCAAAAGATTATTTGTGACGTTTCACTGC 426
    |||
Db 1748 TCCAAAAAATAAGATCTTTTGTGAATGTGAGCAAAAGATTATTTGTGACGTTTCACTGC 1689

OY 427 TTGGTGTGAGCGGCAATCAGTACTGATTTTGAATTTCAAGTCCAAAGATAGACAGAGGCTTC 486
    |||
Db 1688 TTGGTGTGAGCGGCAATCAGTACTGATTTTGAATTTCAAGTCCAAAGATAGACAGAGGCTTC 1629

OY 487 TCTGACCCCAAGGGGTGACATGTGAGCAGTGCACCTTTTCAGCAGAGAGGGTCAAGTGT 546
    |||
Db 1628 TCTGACCCCAAGGGGTGACATGTGAGCAGTGCACCTTTTCAGCAGAGAGGGTCAAGTGT 1569

    547 GACAAACGGGATTTAAGAAGTACACAGTGGAGTGTGAGAGGGGAGTGGCTGGCCCTCT 606
    |||
Db 1568 GACAAACGGGATTTAAGAAGTACACAGTGGAGTGTGAGAGGGGAGTGGCTGGCCCTCT 1509

OY 607 GCGCAGAGAGACCTTACCATTGAGAGTGTGTGATGCTATTCAAGAGCTCAAGTATGAA 666
    |||
Db 1508 GCGCAGAGAGACCTTACCATTGAGAGTGTGTGATGCTATTCAAGAGCTCAAGTATGAA 1449

OY 667 AACTACACCGACGCTTCTTTCATCAGAGACATCATCAAAACGAGCCACCCCAAAACCTG 726
    |||
Db 1448 AACTACACCGACGCTTCTTTCATCAGAGACATCATCAAAACGAGCCACCCCAAAACCTG 1389

OY 727 CAGGTGAAGCATTTGAAGAAATTTCTCGGACGCTGAGAGTGCAGCTGGGAATTTACCCGACAC 786
    |||
Db 1388 CAGGTGAAGCATTTGAAGAAATTTCTCGGACGCTGAGAGTGCAGCTGGGAATTTACCCGACAC 1329

OY 787 TTGAGACACCCACATTTCTCTCTCTTCCCTGACATTTTGCATACAGGCCCAAGGGCAAGAC 846
    |||
Db 1328 TTGAGACACCCACATTTCTCTCTCTTCCCTGACATTTTGCATACAGGCCCAAGGGCAAGAC 1269

OY 847 AATAGAGAAAGAAAGATAGACTCTGCGTGACAAAGACCTTCAGCCAAAGTGTGTTGCCAC 906
    |||
Db 1268 AATAGAGAAAGAAAGATAGACTCTGCGTGACAAAGACCTTCAGCCAAAGTGTGTTGCCAC 1209

OY 907 AAGATGCCCAAGATCCGCGTGCAAGCCGAGACCGCTACTATAGTTCATCTGTGAGGAC 966
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Db 1208 AAGATGCCCAAGATCCGCGTGCAAGCCGAGACCGCTACTATAGTTCATCTGTGAGGAC 1149
OY 967 TTGGCATCTGTGTC 980
    |||
Db 1148 TTGGCATCTGTGTC 1135
```

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RESULT 9
US-09-917-265-52
; Sequence 52, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917, 265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223, 016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 921
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(921)
; OTHER INFORMATION:
US-09-917-265-52
```

```
Query Match          57.2%; Score 914; DB 10; Length 921;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 914; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 67 ATATGGGAGACTGGAGAAAGATGTTTATGTGTAGACTTGGACTGGACACCTGATGCCCCC 126
    |||
Db 1 ATATGGGAGACTGGAGAAAGATGTTTATGTGTAGACTTGGAGCTGGACACCTGATGCCCCC 60

OY 127 GGAGAAATGCTGTGCTCTCACCCTGCCATACCCCTGAGAGAAATATACATCACTTTGGACCTCA 186
    |||
Db 61 GGAGAAATGCTGTGCTCTCACCCTGCCATACCCCTGAGAGAAATATACATCACTTTGGACCTCA 120

OY 187 GCGCAGAGCAGTGAAGTCTAGTTTGTGTAAACTGTGACCAATCCAAAGTCAAAAGATT 246
    |||
Db 121 GCGCAGAGCAGTGAAGTCTAGTTTGTGTAAACTGTGACCAATCCAAAGTCAAAAGATT 180

OY 247 GGAGATGCTGGCCAGTATACCTGCGCATTAAGAGAGCAAGGTTCTGAGCCGCTCACTCTG 306
    |||
Db 181 GGAGATGCTGGCCAGTATACCTGCGCATTAAGAGAGCAAGGTTCTGAGCCGCTCACTCTG 240

OY 307 TTGATTGACAAAAAAGAGATGGAATTTGGTCCAGTATATCTTAAAGAAACGAAAGAA 366
    |||
Db 241 TTGATTGACAAAAAAGAGATGGAATTTGGTCCAGTATATCTTAAAGAAACGAAAGAA 300

OY 367 TCCAAAAAATAAGATCTTTCTGAATGTGAGCAAAAGATTTCTGTGAGCTTTTCACATGC 426
    |||
Db 301 TCCAAAAAATAAGATCTTTCTGAATGTGAGCAAAAGATTTCTGTGAGCTTTTCACATGC 360

OY 427 TTGGTGTGAGCGGCAATCAGTACTGATTTGAATTTCAAGTCTCAAAAGTACAGAGGCTTC 486
    |||
Db 361 TTGGTGTGAGCGGCAATCAGTACTGATTTGAATTTCAAGTCTCAAAAGTACAGAGGCTTC 420

OY 487 TCTGACCCCAAGGGGTGACATGTGAGAGCAGTACACTTTTCACAGAGAGGGTCAAGTGT 546
    |||
Db 421 TCTGACCCCAAGGGGTGACATGTGAGAGCAGTACACTTTTCACAGAGAGGGTCAAGTGT 480

OY 547 GACAAACGGGATTTAAGAAGTACACAGTGGAGTGTGAGAGGGGAGTGGCTGCCCTCT 606
    |||
Db 481 GACAAACGGGATTTAAGAAGTACACAGTGGAGTGTGAGAGGGGAGTGGCTGCCCTCT 540
```

QY	507	GCCAGAGAGATGCTACCCATTCAGAGTCGTGAGTGTGATGATGCTATTTCAGCAAGCTCAAGTATGAA	565
Db	541	GCCAGAGAGATGCTACCCATTCAGAGTCGTGAGTGTGATGCTATTTCAGCAAGCTCAAGTATGAA	600
QY	667	AACATACACGACCACTCTCTTCATCAGAGACATCATCAAAACCAACCCACCCCAAACTCG	726
Db	601	AACATACACGACCACTCTCTTCATCAGAGACATCATCAAAACCAACCCACCCCAAACTCG	660
QY	727	CAGCTGAAGCCATTTGAAAAATTTCTGCGCAGCTGAGGTCAAGCTGGGAATACCGCCGACAC	786
Db	661	CAGCTGAAGCCATTTGAAAAATTTCTGCGCAGCTGAGGTCAAGCTGGGAATACCGCCGACAC	720
QY	787	TGGAGCACCCCACTTCCTACTCTCCCTGACATTTGTCATACAGGCTCCAGGCTCAAGAAC	846
Db	721	TGGAGCACCCCACTTCCTACTCTCCCTGACATTTGTCATACAGGCTCCAGGCTCAAGAAC	780
QY	847	AATAGACAAAAGAAAGATTACATTCCTGCTGACAAAGACCTCACCAGGCTCGTCTGCCAC	906
Db	781	AATAGACAAAAGAAAGATTACATTCCTGCTGACAAAGACCTCACCAGGCTCGTCTGCCAC	840
QY	907	AAGATGTCGAAGATCCCGCTGTGCAAAGCCGAGACCCGCTACTATATAGTTTCATCTCTGAGCGAC	966
Db	841	AAGATGTCGAAGATCCCGCTGTGCAAAGCCGAGACCCGCTACTATATAGTTTCATCTCTGAGCGAC	900
QY	967	TGGGCATCTCTGTC	980
Db	501	TGGGCATCTCTGTC	914

RESULT 10
US-09-917-265-54/c
; Sequence 54, Application US/09917265
; Patent No. US20020052030A1

```

: GENERAL INFORMATION:
: APPLICANT: Mondor, Inc., Ramani S.
: APPLICANT: borroughs, Karen L.
: TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NOCLETIC ACID MOLECULES AND USES THEREOF
: FILE REFERENCE: 1M-5
: CURRENT APPLICATION NUMBER: US/09/917,265
: CURRENT FILING DATE: 2001-07-27
: PRIOR APPLICATION NUMBER: 60/223,016
: PRIOR FILING DATE: 2000-08-04
: NUMBER OF SEQ ID NOS: 105
: SOFTWARE: PatcIn version 3.1
: SEQ ID NO 54
: LENGTH: 921
: TYPE: DNA
: ORGANISM: Canis familiaris
: 5'-09-917-265-54

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Query Match	57.2%	Score 914	PB 10	Length 921
Best Local Similarity	100.0%	Pred. No. 0		
Matches 914	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY	67	ATATGGCAACTGGGAAAGATGTTATGTTGTAGAGTTGACATGGCACCCTGATGGCCCC	126
Db	521	ATATGGCAACTGGGAAAGATGTTATGTTGTAGAGTTGACATGGCACCCTGATGGCCCC	862
QY	127	GGAGAAATAGTGGTCCCTCAGCTGCCATACCCCTGAGAGATAGATCACTTGGACCTCA	186
Db	861	GGAGAAATAGTGGTCCCTCAGCTGCCATACCCCTGAGAGATAGATCACTTGGACCTCA	802
QY	187	GCGTAGAGAGTAGTAGAGTCCTAGCTTTGCTGTAAGACTGTGACCATCCCAAGTCAAGAATTT	245
Db	801	GCGTAGAGAGTAGTAGAGTCCTAGCTTTGCTGTAAGACTGTGACCATCCCAAGTCAAGAATTT	742
QY	247	GGACATGCTTGGCCGTTTACTGTGCATTAAGAGGCGAAGCTTCGAGGCGGCTGCATGCTG	306
Db	741	GGACATGCTTGGCCGTTTACTGTGCATTAAGAGGCGAAGCTTCGAGGCGGCTGCATGCTG	682
QY	307	TTGATTCACAAAAGAAGATGGAATTTGGTCCACTGATATTCCTTAAAGAACGAAGAAGAA	366
Db	681	TTGATTCACAAAAGAAGATGGAATTTGGTCCACTGATATTCCTTAAAGAACGAAGAAGAA	622

QY	367	TCGAAATAATAGCATCTTCTTCTGAAATGTGAGGCCAAAGAAATTTATCTGTGACCTTTCCACATGC	426
Db	621	TTCCAAAATAATAGATCTCTTCTCTGAAATGTGAGGCCAAAGAAATTTATCTGTGACCTTTCCACATGC	562
QY	427	TGTGTGGCTGACGGCATTCACTAGTACGATTTTGAATTTAGTGTCTCAAAAGTATACAGAGGCTTC	486
Db	561	TGTGTGGCTGACGGCATTCACTAGTACGATTTTGAATTTAGTGTCTCAAAAGTATACAGAGGCTTC	502
QY	487	TTCTGACCTCCCAAGGGGTGCATCTGTGAGAGCAGTGCACCTTTTCACGAGAGAGGGTCCAGAGTG	546
Db	501	TTCTGACCTCCCAAGGGGTGCATCTGTGAGAGCAGTGCACCTTTTCACGAGAGAGGGTCCAGAGTG	442
QY	547	GACCAACAGCGATTTAATCAAGTACACAGTGTGAGTGTAGAGAGGGCAGTGGCTGCTCCCTCT	606
Db	441	GACCAACAGCGATTTAATCAAGTACACAGTGTGAGTGTAGAGAGGGCAGTGGCTGCTCCCTCT	382
QY	607	GCCGAGGAGACCTTAACCATTCAGAGTGTGTGTGATGCTATTGCAACAGTCCAGTATGAA	666
Db	381	GCCGAGGAGACCTTAACCATTCAGAGTGTGTGTGATGCTATTGCAACAGTCCAGTATGAA	322
QY	667	AACCTACACCAGCAGCTTCTTCATCAGAGACATCTCAAAACCAGACCACCCACAACCTTG	726
Db	321	AACCTACACCAGCAGCTTCTTCATCAGAGACATCTCAAAACCAGACCACCCACAACCTTG	262
QY	727	CAGCTGAAGCCATTGAAATAATTTCTCGGACACTGAGAGGTCAAGTGGGAAATCCCTCGACACC	786
Db	261	CAGCTGAAGCCATTGAAATAATTTCTCGGACACTGAGAGGTCAAGTGGGAAATCCCTCGACACC	202
QY	787	TGGAGCACCCCAACATTTCTCTACTTCTCCCTGACATTTTTCATACAGGCCCAAGGCCAAGAAC	846
Db	201	TGGAGCACCCCAACATTTCTCTACTTCTCCCTGACATTTTTCATACAGGCCCAAGGCCAAGAAC	142
QY	847	AATACAGAAAGAAAGATAGACCTCTGGGTGTGACAAAGACCTCAGTCCAAGTCTGTGTGCCAC	906
Db	141	AATACAGAAAGAAAGATAGACCTCTGGGTGTGACAAAGACCTCAGTCCAAGTCTGTGTGCCAC	82
QY	907	AAGCATGCTCAAGATTCGGGTGTCAAGACCCGAGACCGCTACTATAGTTATCTCTGTGACGAC	966
Db	81	AAGCATGCTCAAGATTCGGGTGTCAAGACCCGAGACCGCTACTATAGTTATCTCTGTGACGAC	22
QY	967	TGGGCATCTGTGTC	980
Db	21	TGGGCATCTGTGTC	8

RESULT 11
US-09-917-265-49
; Sequence 49, Application US/09917265
; Patent No. US20020052030A1

```

: GENERAL INFORMATION:
: APPLICANT: Wonderling, Ramani S.
: TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
: FILE REFERENCE: 18-5
: CURRENT APPLICATION NUMBER: US/09/917.265
: CURRENT FILING DATE: 2001-07-27
: PRIOR APPLICATION NUMBER: 60/223,016
: PRIOR FILING DATE: 2000-08-04
: NUMBER OF SEQ ID NOS: 109
: SOFTWARE: Patentin version 3.1
: SEQ ID NO 49
: LENGTH: 591
: TYPE: DNA
: ORGANISM: Canis familiaris
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)..(591)
: OTHER INFORMATION:
: US-09-917-265-49
Query Match 30.9%; Score 494; DB 10; Length 591;
Best Local Similarity 100.0%; Pred. No. 11e-252;

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Matches 494:  Conservative 0:  Mismatches 0:  Indels 0:  Gaps 0:
QY 1076 TGAGAGCCGTCAGCAACAGCGCTTCAGAAAGCCAGACAAACTCTAGAAATTATATTCCTGCA 1135
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Db 68 TGAGAGCCGTCAGCAACAGCGCTTCAGAAAGCCAGACAAACTCTAGAAATTATATTCCTGCA 127
QY 1136 CTTCCGAAGAGATTGATCATGAAGATATCACAAGAGATAAACCCAGACAGTGGAGGCT 1195
    |||
Db 128 CTTCCGAAGAGATTGATCATGAAGATATCACAAGAGATAAACCCAGACAGTGGAGGCT 187
QY 1196 GCTTACCACTGGAATTAACCATGATGAGAGTGGCTGGCTCCAGAGAGATCTCTTGA 1255
    |||
Db 188 GCTTACCACTGGAATTAACCATGATGAGAGTGGCTGGCTCCAGAGAGATCTCTTGA 247
QY 1256 TAACCTAACGGAGATTGCTGGCTCTGGAAGGCTCTTTTATGACGGTCTGTGCTTTA 1315
    |||
Db 248 TAACCTAACGGAGATTGCTGGCTCTGGAAGGCTCTTTTATGACGGTCTGTGCTTTA 307
QY 1316 GCAGCATCTATGAGACCTTGAAGATGTACAGATGGAATTCAAGGCCATGAACGCAAGC 1375
    |||
    308 GCAGCATCTATGAGACCTTGAAGATGTACAGATGGAATTCAAGGCCATGAACGCAAGC 367
QY 1376 TTTTATGATGCCAAGAGCGATCTTTGTGATCAAAACATGCTGACAGCTATGCAAT 1435
    |||
Db 368 TTTTATGATGCCAAGAGCGATCTTTGTGATCAAAACATGCTGACAGCTATGCAAT 427
QY 1436 AGCTGTACAGGCCCTGAATTTCAACAGTGTGACTGTGCACAGAAATCTCTTGAAG 1495
    |||
Db 428 AGCTGTACAGGCCCTGAATTTCAACAGTGTGACTGTGCACAGAAATCTCTTGAAG 487
QY 1496 AGCCGATTTTATATAAACTAAATCAAGCTGTGATCTTCTATGCTTTGACAATTC 1555
    |||
Db 488 AGCCGATTTTATATAAACTAAATCAAGCTGTGATCTTCTATGCTTTGACAATTC 547
QY 1556 GTGCGGTGACCATC 1569
    |||
Db 548 GTGCGGTGACCATC 561

RESULT 12
US-09-917-265-51/c
: Sequence 51, Application US/09917265
: Patent No. US20020052030A1
: GENERAL INFORMATION:
: APPLICANT: Wonderling, Ramani S.
: APPLICANT: Boroughs, Karen L.
: TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
: FILE REFERENCE: IM-5
: CURRENT APPLICATION NUMBER: US/09/917,265
: PRIOR APPLICATION NUMBER: 2001-07-27
: PRIOR FILING DATE: 2000-08-04
: NUMBER OF SEQ ID NOS: 109
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 51
: LENGTH: 591
: TYPE: DNA
: ORGANISM: Canis familiaris
US-09-917-265-51

Query Match 30.9%; Score 494: DB 10: Length 591:
Best Local Similarity 100.0%; Pred. No. 1,1e-252:
Matches 494:  Conservative 0:  Mismatches 0:  Indels 0:  Gaps 0:
QY 1076 TGAGAGCCGTCAGCAACAGCGCTTCAGAAAGCCAGACAAACTCTGAATTATATTCCTGCA 1135
    |||
Db 524 TGAGAGCCGTCAGCAACAGCGCTTCAGAAAGCCAGACAAACTCTGAATTATATTCCTGCA 465
QY 1136 CTTCCGAAGAGATTGATCAAGATATCACAAGAGATAAACCCAGACAGTGGAGGCT 1195
    |||
Db 464 CTTCCGAAGAGATTGATCAAGATATCACAAGAGATAAACCCAGACAGTGGAGGCT 405
QY 1196 GCTTACCACTGGAATTAACCATGATGAGAGTGGCTGGCTTCAGAGAGATCTCTTGA 1255
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Db 404 GCTTACCACTGGAATTAACCATGATGAGAGTGGCTGGCTTCAGAGAGATCTCTTGA 345
QY 1256 TAACCTAACGGAGATTGCTGGCTCTGGAAGGCTCTTTTATGACGGTCTGTGCTTTA 1315
    |||
Db 344 TAACCTAACGGAGATTGCTGGCTCTGGAAGGCTCTTTTATGACGGTCTGTGCTTTA 285
QY 1316 GCAGCATCTATGAGACCTTGAAGATGTACAGATGGAATTCAAGGCCATGAACGCAAGC 1375
    |||
Db 284 GCAGCATCTATGAGACCTTGAAGATGTACAGATGGAATTCAAGGCCATGAACGCAAGC 225
QY 1376 TTTTATGATGCCAAGAGCGATCTTTGTGATCAAAACATGCTGACAGCTATGCAATG 1435
    |||
Db 224 TTTTATGATGCCAAGAGCGATCTTTGTGATCAAAACATGCTGACAGCTATGCAATG 165
QY 1436 AGCTGTACAGGCCCTGAATTTCAACAGTGTGACTGTGCACAGAAATCTCTTGAAG 1495
    |||
Db 164 AGCTGTACAGGCCCTGAATTTCAACAGTGTGACTGTGCACAGAAATCTCTTGAAG 105
QY 1496 AGCCGATTTTATATAAACTAAATCAAGCTGTGATCTTCTATGCTTTGACAATTC 1555
    |||
Db 104 AGCCGATTTTATATAAACTAAATCAAGCTGTGATCTTCTATGCTTTGACAATTC 45
QY 1556 GTGCGGTGACCATC 1569
    |||
Db 44 GTGCGGTGACCATC 31

RESULT 13
US-09-917-265-46
: Sequence 46, Application US/09917265
: Patent No. US20020052030A1
: GENERAL INFORMATION:
: APPLICANT: Wonderling, Ramani S.
: APPLICANT: Boroughs, Karen L.
: TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
: FILE REFERENCE: IM-5
: CURRENT APPLICATION NUMBER: US/09/917,265
: PRIOR APPLICATION NUMBER: 2001-07-27
: PRIOR FILING DATE: 2000-08-04
: NUMBER OF SEQ ID NOS: 109
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 46
: LENGTH: 666
: TYPE: DNA
: ORGANISM: Canis familiaris
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)..(666)
: OTHER INFORMATION:
US-09-917-265-46

Query Match 30.9%; Score 494: DB 10: Length 666:
Best Local Similarity 100.0%; Pred. No. 1,1e-252:
Matches 494:  Conservative 0:  Mismatches 0:  Indels 0:  Gaps 0:
QY 1076 TGAGAGCCGTCAGCAACAGCGCTTCAGAAAGCCAGACAAACTCTGAATTATATTCCTGCA 1135
    |||
Db 143 TGAGAGCCGTCAGCAACAGCGCTTCAGAAAGCCAGACAAACTCTGAATTATATTCCTGCA 202
QY 1136 CTTCCGAAGAGATTGATCAAGATATCACAAGAGATAAACCCAGACAGTGGAGGCT 1195
    |||
Db 203 CTTCCGAAGAGATTGATCAAGATATCACAAGAGATAAACCCAGACAGTGGAGGCT 262
QY 1196 GCTTACCACTGGAATTAACCATGATGAGAGTGGCTGGCTTCAGAGAGATCTCTTGA 1255
    |||
Db 263 GCTTACCACTGGAATTAACCATGATGAGAGTGGCTGGCTTCAGAGAGATCTCTTGA 322
QY 1256 TAACCTAACGGAGATTGCTGGCTCTGGAAGGCTCTTTTATGACGGTCTGTGCTTTA 1315
    |||
Db 323 TAACCTAACGGAGATTGCTGGCTCTGGAAGGCTCTTTTATGACGGTCTGTGCTTTA 382
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QY 1316 GCAGATC/TATGAGAGCTTGAGATGTACCAAGATGAAATTCAG:CCATGAACGGCAAGC 1375
|||||
DB 383 GCAGATCTATGAGAGCTTGAGAGATGTACCAAGATGAAATTCAG:CCATGAACGGCAAGC 442
QY 1376 TTTTAATGATCCAGAGAGAGATCTTCTGATCAAAAGATG:TCGACAGCTATGATG 1435
|||||
DB 443 TTTTAATGATCCAGAGAGAGATCTTCTGATCAAAAGATG:TCGACAGCTATGATG 502
QY 1436 AGCTTTACAGGCGCTGAAATTTCAAGACTGTGATGTGCGCACAGAAATCTCCCTTGAAG 1495
|||||
DB 503 AGCTTTACAGGCGCTGAAATTTCAAGACTGTGATGTGCGCACAGAAATCTCCCTTGAAG 562
QY 1496 AGCGGATTTTATAAACTAAATCAAGCTCTGTGATCTTCTGATGCTTTCAGATTC 1555
|||||
DB 563 AGCGGATTTTATAAACTAAATCAAGCTCTGTGATCTTCTGATGCTTTCAGATTC 622
QY 1556 GTGCGGTGACCATC 1569
|||||
DB 623 GTGCGGTGACCATC 636
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RESULT 14

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US-09-917-265-48/c
: Sequence 48, Application US/09917265
: Patent No. US20020052030A1
: GENERAL INFORMATION:
: APPLICANT: Wonderling, Ramani S.
: APPLICANT: Boroughs, Karen L.
: TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
: FILE REFERENCE: 1M-5
: CURRENT APPLICATION NUMBER: US/09/917,265
: PRIOR FILING DATE: 2001-07-27
: PRIOR APPLICATION NUMBER: 60/223,016
: NUMBER OF SEQ ID NOS: 109
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 48
: LENGTH: 666
: TYPE: DNA
: ORGANISM: Canis familiaris
US-09-917-265-48
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Query Match Best Local Similarity 100.0%; Score 494; DB 10; Length 666;

Matches 494; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1076 TGAGAGCCGTGAGCAACAGCGCTTCAGAGGCCAGACAACTCTAGAAATTAATTCCTGCA 1135
|||||
DB 524 TGAGAGCCGTGAGCAACAGCGCTTCAGAGGCCAGACAACTCTAGAAATTAATTCCTGCA 465
QY 1136 CTTCGGAAAGATTCATGATGATGATATCAACAAAGATTAACCGCAGCTGGAGGCT 1195
|||||
DB 464 CTTCGGAAAGATTCATGATGATGATATCAACAAAGATTAACCGCAGCTGGAGGCT 405
QY 1196 GCTTACCACTGGAATTTAAGCATGAGATGCTGCTGCTTCAGAGAGATCTCTTTGA 1255
|||||
DB 404 GCTTACCACTGGAATTTAAGCATGAGATGCTGCTGCTTCAGAGAGATCTCTTTGA 345
QY 1256 TAACCTAACGGAGTTGCTGCGCTCTGGAAGGCCCTTTTATGACGCTCTGTGCTTA 1315
|||||
DB 344 TAACCTAACGGAGTTGCTGCGCTCTGGAAGGCCCTTTTATGACGCTCTGTGCTTA 285
QY 1316 GCAGCATCTATGAGAGCTTGAAAGATGTACGAGATGGAATTTAAGGCCATGAACGCAAGC 1375
|||||
DB 284 GCAGCATCTATGAGAGCTTGAAAGATGTACGAGATGGAATTTAAGGCCATGAACGCAAGC 225
QY 1376 TTTTAATGATCCAGAGAGAGATCTTCTGATCAAAAGATG:TCGACAGCTATGATG 1435
|||||
DB 224 TTTTAATGATCCAGAGAGAGATCTTCTGATCAAAAGATG:TCGACAGCTATGATG 165
QY 1436 AGCTTTACAGGCGCTGAAATTTCAAGACTGTGATGTGCGCACAGAAATCTCCCTTGAAG 1495
|||||
DB 164 AGCTTTACAGGCGCTGAAATTTCAAGACTGTGATGTGCGCACAGAAATCTCCCTTGAAG 105
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QY 1496 AGCGGATTTTATAAACTAAATCAAGCTCTGTGATCTTCTGATGCTTTCAGATTC 1555
|||||
DB 104 AGCGGATTTTATAAACTAAATCAAGCTCTGTGATCTTCTGATGCTTTCAGATTC 45
QY 1556 GTGCGGTGACCATC 1569
|||||
DB 44 GTGCGGTGACCATC 31
```

RESULT 15

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US-09-917-265-104
: Sequence 104, Application US/09917265
: Patent No. US20020052030A1
: GENERAL INFORMATION:
: APPLICANT: Wonderling, Ramani S.
: APPLICANT: Boroughs, Karen L.
: TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
: FILE REFERENCE: 1M-5
: CURRENT APPLICATION NUMBER: US/09/917,265
: PRIOR FILING DATE: 2001-07-27
: PRIOR APPLICATION NUMBER: 60/223,016
: NUMBER OF SEQ ID NOS: 109
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 104
: LENGTH: 1455
: TYPE: DNA
: ORGANISM: Canis familiaris
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (232)..(897)
: OTHER INFORMATION:
US-09-917-265-104
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Query Match Best Local Similarity 100.0%; Score 494; DB 10; Length 1455;

Matches 494; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1076 TGAGAGCCGTGAGCAACAGCGCTTCAGAGGCCAGACAACTCTAGAAATTAATTCCTGCA 1135
|||||
DB 374 TGAGAGCCGTGAGCAACAGCGCTTCAGAGGCCAGACAACTCTAGAAATTAATTCCTGCA 433
QY 1136 CTTCGGAAAGATTCATGATGATGATATCAACAAAGATTAACCGCAGCTGGAGGCT 1195
|||||
DB 434 CTTCGGAAAGATTCATGATGATGATATCAACAAAGATTAACCGCAGCTGGAGGCT 493
QY 1196 GCTTACCACTGGAATTTAAGCATGAGATGCTGCTGCTTCAGAGAGATCTCTTTGA 1255
|||||
DB 494 GCTTACCACTGGAATTTAAGCATGAGATGCTGCTGCTTCAGAGAGATCTCTTTGA 553
QY 1256 TAACCTAACGGAGTTGCTGCGCTCTGGAAGGCCCTTTTATGACGCTCTGTGCTTA 1315
|||||
DB 554 TAACCTAACGGAGTTGCTGCGCTCTGGAAGGCCCTTTTATGACGCTCTGTGCTTA 613
QY 1316 GCAGCATCTATGAGAGCTTGAAAGATGTACGAGATGGAATTTAAGGCCATGAACGCAAGC 1375
|||||
DB 614 GCAGCATCTATGAGAGCTTGAAAGATGTACGAGATGGAATTTAAGGCCATGAACGCAAGC 673
QY 1376 TTTTAATGATCCAGAGAGAGATCTTCTGATCAAAAGATGCTGACAGCTATGATG 1435
|||||
DB 674 TTTTAATGATCCAGAGAGAGATCTTCTGATCAAAAGATGCTGACAGCTATGATG 733
QY 1436 AGCTTTACAGGCGCTGAAATTTCAAGACTGTGATGTGCGCACAGAAATCTCCCTTGAAG 1495
|||||
DB 734 AGCTTTACAGGCGCTGAAATTTCAAGACTGTGATGTGCGCACAGAAATCTCCCTTGAAG 793
QY 1496 AGCGGATTTTATAAACTAAATCAAGCTCTGTGATCTTCTGATGCTTTCAGATTC 1555
|||||
DB 794 AGCGGATTTTATAAACTAAATCAAGCTCTGTGATCTTCTGATGCTTTCAGATTC 853
QY 1556 GTGCGGTGACCATC 1569
|||||
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Db 854 GTGGGTGACCATC 867

Search completed: January 21, 2003, 18:04:59
Job time : 99 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run On: January 21, 2003, 15:46:43 : Search time 1657 Seconds
(without alignments)
15628.596 Million cell updates/sec

Title: US-09-917-265-61
Perfect score: 1599
Sequence: 1 atgacccctcgcagcttgg.....tgctctactctgactcttc 1599

Scoring Table: OLI_GCO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

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Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: listing first 1000 summaries

Database :

- FAST:
- 1: em_estba:*
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 - 21: em_ys_vrl:*
 - 22: em_ys_tun:*
 - 23: em_ys_mam:*
 - 24: em_ys_mus:*
 - 25: em_ys_other:*
 - 26: em_ys_pro:*
 - 27: em_ys_trod:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Score	Match	Length	DB	ID	Description
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3	31	1.9	589	9	A1050362	A1050362	nb30a07.r
4	30	1.9	373	12	Bf552757	Bf552757	UI-R-CO-1
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6	26	1.6	342	13	BM257856	BM257856	521721 MA

7	25	1.6	812	12	BG702253	BG702253	602683459
8	22	1.4	529	13	B1725614	B1725614	1031079H1
9	22	1.4	642	13	BM600965	BM600965	170006870
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11	21	1.3	489	17	A2884788	RPCI-23-1	
12	21	1.3	369	17	AQ393691	CITB1-E1-	
13	21	1.3	552	13	BM085578	sa126q11.	
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16	21	1.3	638	13	B1099266	B1099266	TP1_40-G0
17	21	1.3	646	10	BB038225	BB038225	
18	21	1.3	667	13	BJ042592	BJ042592	
19	21	1.3	679	14	B0002107	B0002107	OGG30B21.
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21	21	1.3	777	10	BE033953	BE033953	MG02E08 M
22	21	1.3	975	17	CNS04WT	CNS04WT	
23	20	1.3	136	13	BM140498	BM140498	WHE0484_a
24	20	1.3	167	10	AM472465	AM472465	sa125f02.y
25	20	1.3	173	13	BJ006287	BJ006287	
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27	20	1.3	241	17	A2891891	A2891891	RPCI-24-2
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29	20	1.3	296	13	B1498525	B1498525	sa115c08.
30	20	1.3	305	9	A1441440	A1441440	sa59h11.y
31	20	1.3	316	13	BM522480	BM522480	samp93e09.
32	20	1.3	333	10	AM311474	AM311474	sg40b04.y
33	20	1.3	340	14	BQ770669	BQ770669	UI-M-F10-
34	20	1.3	348	17	AQ373901	AQ373901	RPCI11-14
35	20	1.3	341	13	B1973274	B1973274	sa186c03.
36	20	1.3	346	10	AM164696	AM164696	se76d07.y
37	20	1.3	352	10	BE610397	BE610397	so55b10.y
38	20	1.3	366	13	B1424493	B1424493	saH50g10.
39	20	1.3	374	14	T99581	T99581	ye63d08.r1
40	20	1.3	385	12	BE703854	BE703854	MR2-NN111
41	20	1.3	421	17	AQ673149	AQ673149	HS_-5496_A
42	20	1.3	433	14	BQ610072	BQ610072	sap36g02.
43	20	1.3	436	10	AV792889	AV792889	AV792889
44	20	1.3	439	9	A1442207	A1442207	sa49b01.y
45	20	1.3	475	12	BF704417	BF704417	MT-P-E6-a
46	20	1.3	478	13	B1786422	B1786422	sa136h10.
47	20	1.3	511	9	AA135692	AA135692	z11ic04.r
48	20	1.3	516	17	AQ478437	AQ478437	RPCI-11-2
49	20	1.3	527	17	BH780306	BH780306	fcm0b15f0
50	20	1.3	530	14	BM884387	BM884387	rc10f05.y
51	20	1.3	536	10	AV554146	AV554146	AV554146
52	20	1.3	547	13	B1419150	B1419150	LJNEST35h
53	20	1.3	550	17	B75609	B75609	RPC111-11L1
54	20	1.3	553	14	BQ611351	BQ611351	sap58g05.
55	20	1.3	558	13	B1417713	B1417713	LJNEST34e
56	20	1.3	566	17	BH844788	BH844788	TC3-51M10
57	20	1.3	567	14	BQ985784	BQ985784	OG67L20.y
58	20	1.3	569	17	A2853726	A2853726	2M0157M01
59	20	1.3	581	14	BO508151	BO508151	EST615566
60	20	1.3	598	11	BF060081	BF060081	Hc_d11_11
61	20	1.3	601	9	AA441005	AA441005	LD15736_5
62	20	1.3	604	14	W63576	W63576	zc55n09.r1
63	20	1.3	605	17	AQ544128	AQ544128	RPC1-11-3
64	20	1.3	637	9	A1982112	A1982112	patc.pk007
65	20	1.3	638	10	BB665614	BB665614	sp51g02.y
66	20	1.3	642	10	BE473398	BE473398	sp51g02.y
67	20	1.3	669	10	BB644880	BB644880	BB644880
68	20	1.3	673	13	BM427122	BM427122	potf2n.pk0
69	20	1.3	674	17	BH842473	BH842473	TC3-57N10
70	20	1.3	690	17	A2424475	A2424475	1M0204A12
71	20	1.3	707	14	B0002016	B0002016	OG62g12.y
72	20	1.3	711	14	BO509384	BO509384	EST616799
73	20	1.3	742	13	B1175859	B1175859	EST516942
74	20	1.3	757	13	B1177417	B1177417	EST518362
75	20	1.3	778	10	BE548053	BE548053	601072084
76	20	1.3	855	17	AQ893069	AQ893069	HS_-3072_A
77	20	1.3	859	12	BE737982	BE737982	601572557
78	20	1.3	862	13	B1830737	B1830737	603075132
79	20	1.3	1605	11	AK018149	AK018149	Mus muscu

C 956	18	1.1	608	14	BQ019806	BQ019806 UT-H-ED0-
C 957	18	1.1	609	9	AI323590	AI323590 mp61a10.x
C 958	18	1.1	611	9	AI406469	AI406469 EST234755
C 959	18	1.1	611	10	AV949757	AV949757 AV949757
C 960	18	1.1	611	14	B0636071	B0636071 hb04a08.y
C 961	18	1.1	615	9	AL587333	AL587333 AL587333
C 962	18	1.1	616	12	BE703846	BE703846 MR2-NN11
C 963	18	1.1	616	13	BJ315590	BJ315590 BJ315590
C 964	18	1.1	616	17	CNS030PX	AL256254 Tetradon
C 965	18	1.1	617	10	AV856038	AV856038 AV856038
C 966	18	1.1	617	13	BI665093	BI665093 603287527
C 967	18	1.1	617	13	BI837660	BI837660 603086894
C 968	18	1.1	618	14	BQ704149	BQ704149 946110610
C 969	18	1.1	619	13	BM015809	BM015809 603642075
C 970	18	1.1	621	10	BE047991	BE047991 t245b11.y
C 971	18	1.1	621	17	AO157438	AO157438 nbxb00000
C 972	18	1.1	622	10	AW950177	AW950177 EST362142
C 973	18	1.1	623	10	AW979727	AW979727 EST341350
C 974	18	1.1	624	13	BI719312	BI719312 103104260
C 975	18	1.1	624	13	BM406823	BM406823 EST581150
C 976	18	1.1	625	13	BJ366927	BJ366927 BJ366927
C 977	18	1.1	626	13	BM171650	BM171650 imageqc.5
C 978	18	1.1	627	14	BM758677	BM758677 K-EST00038
C 979	18	1.1	628	17	AZ447992	AZ447992 IM0245323
C 980	18	1.1	630	9	AA501118	AA501118 v197h05.r
C 981	18	1.1	630	17	AZ741434	AZ741434 RPCI-24-1
C 982	18	1.1	632	17	AZ352897	AZ352897 IM0091L03
C 983	18	1.1	633	9	AL677215	AL677215 AL677215
C 984	18	1.1	633	12	BF054495	BF054495 EST439725
C 985	18	1.1	635	17	AQ256700	AQ256700 nbxb00168
C 986	18	1.1	636	14	BM943606	BM943606 UT-M-EH0P
C 987	18	1.1	637	10	AW584220	AW584220 N210191P
C 988	18	1.1	637	12	BF216416	BF216416 601884464
C 989	18	1.1	639	14	BM747664	BM747664 K-EST0022
C 990	18	1.1	641	10	BB665546	BB665546 BB665546
C 991	18	1.1	641	10	BE414268	BE414268 SCU007.H0
C 992	18	1.1	641	12	BE890732	BE890732 601431162
C 993	18	1.1	641	14	BQ609121	BQ609121 BRY-5042
C 994	18	1.1	641	17	BH125092	BH125092 RPCI-24-3
C 995	18	1.1	642	14	BM722659	BM722659 UT-E-E00-
C 996	18	1.1	643	13	BM496426	BM496426 JPCGBR2.1
C 997	18	1.1	643	14	BQ394119	BQ394119 NISC.ng07
C 998	18	1.1	643	17	BM286010	BM286010 CH230-157
C 999	18	1.1	644	10	BE414258	BE414258 SCU007.G0
C1000	18	1.1	644	13	BI433722	BI433722 EST536483

ALIGNMENTS

RESULT 1
BI824638 447 bp mRNA linear EST 04-OCT-2001
LOCUS 603033580F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5175018 5',
DEFINITION
MRNA sequence.
BI824638
BI824638.1 GI:15936188
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 447)
NIH-MGC <http://mgc.ncl.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-f@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be

FEATURES
source
1. 447
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5175018"
/clone_11b="NIH_MGC_115"
/lab_host="DH10B"
/note="Organ: pooled brain, lung, testis; Vector: pcwv-SPORT6; site_1: NotI; site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH MGC Library."

BASE COUNT 149 a 63 c 87 g 148 t
ORIGIN

Query Match 2.6%; Score 41; DB 13; Length 447;
Best Local Similarity 100.0%; Pred. No. 8.6e-10;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1516 AAATCAAGCTCTGACATCTTCTTCATGCTTTCAGCAATTCG 1556
Db 1 AAATCAAGCTCTGACATCTTCTTCATGCTTTCAGCAATTCG 41
|||||

RESULT 2
BI523344 1099 bp mRNA linear EST 29-AUG-2001
LOCUS 603175938T1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5240216 3',
DEFINITION
MRNA sequence.
BI523344
BI523344.1 GI:15348136
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 (bases 1 to 1099)
NIH-MGC <http://mgc.ncl.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-f@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
Plate: LLM11605 row: 1 column: 09
High quality sequence start: 40
High quality sequence stop: 727.
Location/Qualifiers
1. 1099
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5240216"
/clone_11b="NIH_MGC_121"
/lab_host="DH10B"
/note="Organ: brain; Vector: PCWV-SPORT6; site_1: NotI; site_2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and

FEATURES

source

bacteria (Life Technologies) to generate the UI-R-CO library. This procedure has been previously described (Ronald, Lennon and Soares, Genome Research 6: 791-806, 1996).

BASE COUNT 106 a 93 c 89 g 85 t

Query Match 1.9%: Score 30; DB 12; Length 373;
Best Local Similarity 100.0%: Pred. No. 0.00047;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1318 AGCATCTATGAGAGCTTAAGATGACCAG 1347
|||||
Db 98 AGCATCTATGAGAGCTTAAGATGACCAG 127

RESULT 5
LOCUS

BI523569 832 bp mRNA linear EST 29-AUG-2001
603175938F1 NIH_MGC_121 Homo sapiens CDNA clone IMAGE:5240216 5',
mRNA sequence.

ACCESSION BI523569
VERSION BI523569.1 GI:15348361
KEYWORDS EST.
SOURCE human.

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Human.
Homo sapiens
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 832)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LLM1605 row: 1 column: 09
High quality sequence start: 23
High quality sequence stop: 821.
Location/Qualifiers

FEATURES
source 1..832
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5240216"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
fetal brains, female age 20 weeks, female age 24 weeks,
and male age 26 weeks. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
0.7-3.5 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 017. Note:
this is a NIH-MGC Library."

BASE COUNT 220 a 233 c 200 g 179 t

Query Match 1.8%: Score 29; DB 13; Length 832;
Best Local Similarity 100.0%: Pred. No. 0.002;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1141 GAAGAGATTGATCATGAGATATCACAA 1169
|||||
Db 520 GAAGAGATTGATCATGAGATATCACAA 548

RESULT 6
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS

TITLE
JOURNAL
MEDLINE
COMMENT

Bos taurus
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 342)
Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,
G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,
Pettea,G., Holt,L., Karamycheva,S., Liang,F., Quackenbush,J. and
Keefe,J.W.
Sequence evaluation of four pooled-tissue normalized bovine CDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
21180013
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.
PCR primers
FORWARD: AGCAACACGATGACCAT
BACKWARD: GTTTCACGTCACGACG
Plate: 125 row: E column: 18
Seq primer: ATTTAGCTGACACTATAG.
Location/Qualifiers

FEATURES
source 1..342

/organism="Bos taurus"
/db_xref="taxon:9913"
/clone="MARC 3BOV"
/issue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendinosus muscle, and fetal
longissimus muscle."

BASE COUNT 67 a 135 c 74 g 66 t

Query Match 1.6%: Score 26; DB 13; Length 342;
Best Local Similarity 100.0%: Pred. No. 0.057;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1099 CAGAAGCCACAGCAACTCTAGCAATT 1124
|||||
Db 294 CAGAAGCCACAGCAACTCTAGCAATT 319

RESULT 7
LOCUS

DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BG702253 812 bp mRNA linear EST 07-MAY-2001
602683459F1 NIH_MGC_95 Homo sapiens CDNA clone IMAGE:4816118 5',
mRNA sequence.
BG702253
BG702253.1 GI:13973409
EST.
human.
Homo sapiens
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 812)
NIH-MGC http://mgc.nci.nih.gov/.

```

TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1995)
COMMENT    Contact: Robert Strausberg, Ph.D.
           Email: ccgabs-remail.nih.gov
           Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
           cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiroki
           Toshiyuki and Piero Carninci (RIKEN)
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
           DNA Sequencing by: Incyte Genomics, Inc.
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LNL at:
           http://image.llnl.gov
           Plate: L14M10714 row: e column: 15
           High quality sequence stop: 804.

FEATURES
  source
    1..812
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /clone_image="4816118"
    /clone_lib="NIH_MGC_95"
    /issue_type="hippocampus"
    /lab_host="DH10B"
    /note="Organ: brain; Vector: Bluescript (modified
    pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (dgcgg
    ); Oligo-dT primed using primer 5'-TTTTTTTTTTTNN-3',
    size-selected for average insert size 2.5 kb and
    normalized to 10^5. This is a primary library enriched
    for full-length clones and constructed using the
    Cap-trapper method (Carninci, in preparation). Library
    constructed by M. Brownstein (NIH/NHGRI, National
    Institutes of Health). Note: This is a NIH-MGC Library."

BASE COUNT      188 a      245 c      226 g      149 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1095 CACAAAGCCGACCAACTCTAGAAATT 1124
      |||||||
Db 573 CACAAGCCGACCAACTCTAGAAATT 598

RESULT 8
BI725614/c 529 bp mRNA linear EST 19-SEP-2001
LOCUS 1031075H11.Y1 C. reinhardtii CC-1690, Stress II (normalized),
DEFINITION lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
ACCESSION BI725614
VERSION BI725614.1 GI:15701309
KEYWORDS EST.
SOURCE Chlamydomonas reinhardtii.
ORGANISM Chlamydomonas reinhardtii
          Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
          Chlamydomonadaceae; Chlamydomonas.
REFERENCE 1 (bases 1 to 529)
          Grossman, A., Chenu, C.-W., Davies, J., Harris, F., Hauser, C., Lefebvre
          P., McChermott, J.P., Shroyer, J., Sillitow, C. and Stern, D.
          Analyses of the Chlamydomonas reinhardtii Genome: A Model,
          Unicellular System for Analyzing Gene Function and Regulation in
          Vascular Plants. Project: 1031
          Unpublished (2001)
          Contact: Charles Hauser
          DCMR Box 91000
          Duke University
          Durham, NC 27708-1000
          Tel: 919 613 8159
          Fax: 919 613 8177
          Email: chauser@duke.edu.

FEATURES
  source
    1..529
    /organism="Chlamydomonas reinhardtii"
    /strain="CC-1690 wild type mt- 219r"

```

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/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, Stress II (normalized
), Lambda Zap II"
/note="Vector: Bluescript II SK+; Site_1: EcoRI; Site_2:
XhoI; Stress condition II library, constructed by John
Davis and Jeffrey McDermott, combines cDNAs from CC-1690
cells grown to mid-log phase in TAP (NH4+ containing)
and shifted to TAP - NO3- (24hrs); H2 production
conditions (0, 12hr, 24hr) see Melis et al., (2000) Plant
Phys. 122: 127-135; TAP + H2O2 (1, 12, 24 hr); TAP +
sorbitol (1, 2, 6, 24 hr); TAP + Cd (1, 2, 6, 24 hr).
PolyA mRNA was purified from each sample, pooled and cDNA
synthesized. The cDNA was directionally cloned into lambda
Zap II (Stratagene) in the EcoRI (5') and XhoI (3')
sites. pBluescript II SK+ plasmids were excised from the
lambda Zap clones by superinfection with ExSist
(Stratagene) phage. The library was normalized using
method 4 described in Bonaldo et al., (1996) Genome
Research 6: 791-806."

BASE COUNT      103 a      226 c      123 g      77 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 983 CCACTGCGCGCGGCGCGCGCG 1004
      |||||||
Db 396 CCACTGCGCGCGGCGCGCGCG 375

RESULT 9
BM600965 642 bp mRNA linear EST 25-FEB-2002
LOCUS 17000687067149 A.Gam.ad.cDNA.blood1 Anopheles gambiae cDNA clone
DEFINITION 19600449680120 5', mRNA sequence.
ACCESSION BM600965
VERSION 19600449680120 5', mRNA sequence.
KEYWORDS BM600965.1 GI:18899069
SOURCE EST.
ORGANISM African malaria mosquito.
          Anopheles gambiae
          Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
          Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
          Anopheles.
REFERENCE 1 (bases 1 to 642)
          Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L., Charlab
          , R., Collins, F.H., Venter, J.C. and Hoffman, S.L.
          Celera Anopheles gambiae EST project
          Unpublished (2002)
          Contact: Holt R.A.
          Celera Genomics
          45 W. Gude Dr., Rockville, MD 20850, USA
          Tel: 2404533151
          Fax: 2404534580
          Email: HOLTRA@celera.com
          Plate: ND01004B3L row: M column: 02
          Seq primer: M13 Reverse.

FEATURES
  source
    1..642
    /organism="Anopheles gambiae"
    /strain="RSP-ST (Reduced susc. to Permethrin - std.
    chromosome)"
    /db_xref="taxon:7165"
    /clone_image="19600449680120"
    /clone_lib="A.Gam.ad.cDNA.blood1"
    /dev_stage="Adult"
    /lab_host="DH10B"
    /note="Vector: pSport1; Site_1: SalI; Site_2: NotI; Whole
    adult mosquitoes (mixed sex) frozen on liquid nitrogen 24
    hours after human blood feeding. cDNA inserts >500 bp
    cloned directionally into pSport 1. Not I site is 3'.
    Clones available through the Malaria Research and
    Reference Reagent Resource Center (www.malaria.m4.org)"

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BASE COUNT      135 a      193 c      216 g      98 t
ORIGIN
Query Match      1.4%: Score 22; DB 13; Length 642;
Best Local Similarity 100.0%; Pred.No. 8.6;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      983 GCAGTGGTGGCGGTGGCGGCGG 1004
      |||
Db      147 GCAGTGGTGGCGGTGGCGGCGG 168

RESULT 10
AC049786      662 bp      DNA      linear      GSS 02-NOV-2001
LOCUS      Pan troglodytes DNA, clone: PTB-030A07.R, genomic survey sequence.
ACCESSION      AG049786
VERSION      AG049786.1 GI:16586678
KEYWORDS      GSS.
REFERENCE      Pan troglodytes male lymphoblast DNA, clone_11b:PTB Chimpanzee Male
      BAC library clone:PTB-030A07.R.
      Pan troglodytes
      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
ORGANISM
REFERENCE      1
AUTHORS      Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
      Totoki,Y., Watanabe,H. and Sakaki,Y.
      BAC end sequences of library PTB
      Unpublished
      2 (bases 1 to 662)
      Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
      Totoki,Y., Watanabe,H. and Sakaki,Y.
      Direct Submission
      Submitted (02-NOV-2001) Asao Fujiyama, The Institute of Physical
      and Chemical Research (RIKEN), Genomic Sciences Center (GSC):
      1-7-22 Suehiro-cho,Tsukumi-Ku, Yokohama, Kanagawa 230-0045, Japan
      (E-mail:chimpes@gs.c.riken.go.jp, URL:http://hgp.gs.c.riken.go.jp/,
      Tel:81-45-503-9111, Fax:81-45-503-9170)
      Clones are derived from the chimpanzee BAC library PTB This BAC end
      was generated during the R&D process and may have higher chance of
      clone tracking errors.
      PRIMERS
      Sequencing: M13rev
      LIBRARY
      Vector : pKS145
      R.site 1 : SacI
      R.site 2 : SacI.
      Location/Qualifiers
      1..662
      /organism="Pan troglodytes"
      /db_xref="taxon:9598"
      /clone="PTB-030A07.R"
      /sex="male"
      /cell_type="lymphoblast"
      /clone_11b="PTB Chimpanzee Male BAC library"
      118 c      140 g      206 t
BASE COUNT      197 a      118 c      140 g      206 t
ORIGIN
Query Match      1.4%: Score 22; DB 17; Length 662;
Best Local Similarity 100.0%; Pred.No. 8.7;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      307 TTGATTACAAAAAGACATG 328
      |||
Db      345 TTGATTACAAAAAGACATG 366

RESULT 11
AC2884788      369 bp      DNA      linear      GSS 05-MAR-2001
LOCUS      RPCI-23-182A5.TV RPCI-23 Mus musculus genomic clone RPCI-23-182A5,
ACCESSION      DNA sequence.
      A2884788
      A2884788

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VERSION      A2884788.1 GI:13203733
KEYWORDS      GSS.
SOURCE      house mouse.
ORGANISM      Mus musculus.
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
      1 (bases 1 to 369)
AUTHORS      Zhao,S., Nierman,W., Feldblum,T., Malek,J., Shatsman,S., Akiret
      ,B., Levins,M., Moggan,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
      and Fraser,C.M.
      Mouse BAC End Sequences from library RPCI-23
      Unpublished (1999)
      Other_GSSs: RPCI-23-182A5.TJ
      Contact: Shaying Zhao
      Department of Eukaryotic Genomics
      The Institute for Genomic Research
      9712 Medical Center Dr., Rockville, MD 20850, USA
      Tel: 301 838 0200
      Fax: 301 838 0208
      Email: szhao@tigr.org
      Clones are derived from the mouse BAC library RPCI-23. For BAC
      library availability, please contact Pieter de Jong
      (pdejong@mail.cho.org). Clones may be purchased from BACPAC
      Resources (http://www.choi.org/bacpac/orderingframe.htm). BAC end
      page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
      Plate: 182 row: A column: 5
      Seq primer: 17
      Class: BAC ends.
FEATURES
      source
      1..369
      Location/Qualifiers
      /organism="Mus musculus"
      /strain="C57BL/6J"
      /db_xref="taxon:10090"
      /clone="RPCI-23-182A5"
      /clone_11b="RPCI-23"
      /sex="Female"
      /lab_host="DH10B"
      /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site:1;
      EcoRI; Site:2; EcoRI; Female C57BL/6J mouse kidney and/or
      brain genomic DNA was isolated and partially digested
      with a combination of EcoRI and EcoRI Methylase. Size
      selected DNA was cloned into the pBACe3.6 vector at the
      EcoRI sites. The ligation products were transformed into
      DH10B electrocompetent cells (BRL Life Technologies)."
BASE COUNT      97 a      76 c      86 g      110 t
ORIGIN
Query Match      1.3%: Score 21; DB 17; Length 369;
Best Local Similarity 100.0%; Pred.No. 24;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      484 TTCTGTACCCCAAGCGTG 504
      |||
Db      121 TTCTGTACCCCAAGCGTG 141

RESULT 12
AO393691/C      489 bp      DNA      linear      GSS 06-MAR-1999
LOCUS      CITBI-EI-2544N3.TF CITBI-EI Homo sapiens genomic clone 2544N3, DNA
ACCESSION      sequence.
      AO393691
      AO393691.1 GI:4364714
      GSS.
VERSION      AO393691.1
KEYWORDS      human.
SOURCE      Homo sapiens
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
      1 (bases 1 to 489)
REFERENCE      Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
      Venter,J.C.
      Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
      Map Building

```

JOURNAL
COMMENT Unpublished (1997)
Other CSSS: CITBI-EI-2544N3.TR
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
5712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0260
Fax: 301 838 0208
Email: hbe@lifer.org

Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/human/bac_end_search/bac_end_search.html
Seq primer: M13-21
Class: BAC ends.

FEATURES

Source
1..489
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2544N3"
/clone_lib="CITBI-EI"
/sex="male"
/cell_type="sperm"
/note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2: EcoRI;
Caltech Human BAC Library D"
BASE COUNT 148 a 97 c 103 g 140 t 1 others
ORIGIN

Query Match 1.3%; Score 21; DB 17; Length 489;
Best local similarity 100.0%; Pred. No. 25;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1220 ATGACGTTGCTGCTGCCA 1240
|||||
DB 441 ATGACGTTGCTGCTGCCA 421

RESULT 13
BM085578/c 552 bp mRNA linear EST 19-NOV-2001
LOCUS
Definition: Scl26b11.y1 Gm-cl066 Glycine max cDNA clone SOYBEAN CLONE ID:
Gm-cl066-4149 5' similar to TR:Q9SE97 Q9SE97 FORMIN-LIKE PROTEIN
AHP1.; mRNA sequence.
ACCESSION BM085578
VERSION
KEYWORDS
SOURCE BM085578.1 GI:16596206
EST.

ORGANISM soybean.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eustoids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.

REFERENCE 1 (bases 1 to 552)

AUTHORS

Shoemaker, R., Keim, P., Vodka, L., Erpelting, J., Corvelli, V., Rhana,
A., Bolla, B., Maria, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,
Wylie, T., Underwood, K., Stepien, M., Theising, R., Allen, K., Bowers,
Y., Person, B., Sweller, T., Gibbons, M., Pape, D., Harvey, N., Schurk,
R., Ritzer, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann,
R., Waterston, R., and Wilson, R.
Public Soybean EST Project

TITLE Unpublished (1999)

JOURNAL

COMMENT Contact: Shoemaker R/Public Soybean EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@wustl.edu

This clone is available through: Resgen, Invitrogen Corp. 2130

South Memorial Parkway Huntsville, AL 35801 For further information

call: (800)-533-4365 or contact: csh@resgen.com web site:

www.resgen.com

High quality sequence stop: 424.

Location/Qualifiers

FEATURES

source

1..552
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-cl066-4149"
/clone_lib="Gm-cl066"
/tissue_type="leaf and shoot tip, salt stressed, 2 week
old seedling"
/lab_host="DH10B"
/note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
XhoI; The cDNA library was constructed from mRNA isolated
from unexpanded leaves and the shoot tips of 2 week old
seedlings from the cultivar Williams. The 2 week old
seedlings were salt stressed in a solution of 500mM NaCl
for 3 days prior to harvesting. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(dT) sequence with a XhoI restriction site. EcoRI
adapters were ligated to the blunt-ended cDNA fragments
followed by XhoI digestion. The cDNA fragments were
directionally cloned into the EcoRI-XhoI restriction site
of the pBluescript vector. The ligated cDNA fragments were
transformed into DH10B host cells (GibcoBRL). This library
was constructed in the laboratory of Dr. Randy
Shoemaker."

BASE COUNT 132 a 144 c 135 g 141 t
ORIGIN
Query Match 1.3%; Score 21; DB 13; Length 552;
Best local similarity 100.0%; Pred. No. 27;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 964 CAGTGGTGGCGGTGGCGCGG 1004
|||||
DB 89 CAGTGGTGGCGGTGGCGCGG 69

RESULT 14
BJ030774 564 bp mRNA linear EST 05-DEC-2001
LOCUS
Definition: BJ030774 NIBB Mochi normalized Xenopus neurula library Xenopus
laevis cDNA clone XL005C01 5', mRNA sequence.
ACCESSION BJ030774
VERSION
KEYWORDS
SOURCE BJ030774.1 GI:17377868
EST.

ORGANISM African clawed frog.
Xenopus laevis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus.

REFERENCE 1 (bases 1 to 564)

AUTHORS

Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and Kohara,
Y.
Expressed genes in X. laevis embryo
Unpublished (2001)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tsuhin@genes.nig.ac.jp.

FEATURES

Source

1..564
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="XL005C01"
/clone_lib="NIBB Mochi normalized Xenopus neurula
library"
/tissue_type="whole embryo"
/dev_stage="stage 15"
/note="Vector: pBSRN3; Site_1: NotI; Site_2: EcoRI; cDNAs
were oligo-dT primed and directionally cloned. Staging
according to Nieuwkoop and Faber. Library is subtracted
and was constructed by N. Garrett and A.M. Zorn,

High quality sequence stop: 424.

Location/Qualifiers

FEATURES

BASE COUNT 138 a 148 c 136 g 142 t
 ORIGIN (Wellcome/CRC Institute). "

Query Match 1.3%; Score 21; DB 13; Length 564;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 GATGCTGGCAGTATACCTGC 270
 ||||||||||||||||||
 Db 178 GATGCTGGCAGTATACCTGC 198

RESULT 15
 BJ032049

LOCUS BJ032049 571 bp mRNA linear EST 05-DEC-2001
 DEFINITION laevis cDNA clone XL015h03 5', mRNA sequence.
 ACCESSION BJ032049
 VERSION BJ032049.1 GI:17375617
 WORDS EST.
 SOURCE African clawed frog.
 ORGANISM Xenopus laevis

REFERENCE 1 (bases 1 to 571)
 AUTHORS Kikayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-I, T. and Kohara, Y.
 TITLE Expressed genes in X. laevis embryo
 JOURNAL Unpublished (2001)
 COMMENT Contact: Tadasi Shin-I
 Center For Genetic Resource Information
 National Institute of Genetics
 111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshin@genes.nig.ac.jp.
 Location/Qualifiers

FEATURES
 source

1..571
 /organism="Xenopus laevis"
 /db_xref="taxon:8355"
 /clone_id="XL015h03"
 /library="NIBB Mochii normalized Xenopus neurula library"
 /tissue_type="whole embryo"
 /dev_stage="stage 15"
 /note="vector: pBSRN3; Site_1: NotI; Site_2: EcoRI; CDNAS were oligo-dT primed and directionally cloned. Staging according to Nieuwkoop and Faber. Library is subtracted and was constructed by N. Garrett and A.M. Zorn, (Wellcome/CRC Institute). "

BASE COUNT 142 a 142 c 143 g 144 t
 ORIGIN

Query Match 1.3%; Score 21; DB 13; Length 571;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 GATGCTGGCAGTATACCTGC 270
 ||||||||||||||||||
 Db 140 GATGCTGGCAGTATACCTGC 160

Search completed: January 21, 2003, 17:11:54
 Job time : 1726 secs